

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGACGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTGGTTGTTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTGAAGTGGTGGTGCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCATTTCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGT
ACAACACTACTTACTGATAGACAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACCTACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTGTTAGATCG
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACAAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
GTTCCCTCTTTCCGGGGTCTCACCAGAAGAGGTTCTTGCGGGTCCGCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCGCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGTCTGCTGTCATCTACTTTGCTCTGGAATGTCTAAATGTTTC
TGTAGCAGAAAAACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGACTG
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCITGGGAGGCCAGCCAGCTTTACCTGCTGTTCTCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCTTGAGCAATGGGCTCTGTCTCGCTGGCCCTGCCCTGGA
AATAAGGAGCCT**CTAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

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FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

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GLGGEVPGSHQGPDYPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAATTTTCATGAAGTACCAAGAGGACACCATCTT
 CTTGTATTATACAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCCTCCTAATCCTCTGTGGTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
 AGAACTTTTGATAAAAAGGATTTTCATGTAATCGTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTCCCGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
 ATCGTTGGAGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACGAGGATTGTTCAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAAAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAGAGATGCCAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCCACAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTATCTGCTCCAACCTGGACTCATTTAGA
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 CTCGAAGTTTCTTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
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FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVS SVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVI EKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCTGACGCGCGCAGTGGGCGGGGCCCTTGGGCCGTGCGCCACCAGT
 GTAGTCATGTACCCACGCCCGCCGCGCCTCATCGGACATTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTTGACAAACAGCAAGAGTTGGCGCGGGCGCTCGTGCTGGAGGAATGGA
 AGCAACTGTCGAGATTGCGAGCGGAATATGATTCTCTTCTCCTTGCCCTTCTGCTTTTCTGT
 GGACTCCTCTTACATCAACTTGGCTGACCATTGAAAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAACACGCAAAATCCACCGTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGTCACAGAAGACAAA
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 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACCACTGTCATCTGAACATCGCCAGAGGGCGTGATTGACGTCTTCTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTCACT
 GAGTGGTTTGGCCCTCGGTCTCACACTGATCGACGCGCTGGACACCACTGTGGATCTTGGGT
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 TGGACGTCAACCTGTTTGAGAGCAGGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGACAGCCTCTTCTCAGGAAAGCTGAGGATTTGGAAATCGGCTAATGCCTGC
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 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAAGCTTCACTGAGTTGGATTCGG
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 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGTGGAAAGCTACGTGGA
 AGCCATCGAGGGTGTGAGAAGCAGCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG
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 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTATCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGTGCGGCCAGAGACCGCTGGAGAGCCTGTTCTACCTGACCCGCTCACAGGGGA
 CCGCAAAATACCAGGATCGGGCTGGGAGATTCTGCAGAGCTTCAAGCCGATTCACCGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCTGGACGCGCTACGTGTTCAACACCGAAGCCACCTCTGCCATATCT
 GGACCCCTGCC**TAGG**GTGGATGGCTGCTGGTGTGGGGACTTGGGTGGGCAGAGGACCTTG
 CTGGGTCTGTGGCATTTTCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCT
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 GGCGCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTGCTTCTC
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 GAGGGGGGCTTCGAGGTGGTCCCTGCTACTGGGTTGACCGAGTGGACAGCCAGGTTGCAGC
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 CTCAGAGGCGCTGAGGCTCAGGGCTGGCTGCTGTTTACAAGCTGAGCTCAGGATCCTC
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FIGURE 10

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IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTTELPSRRAEVPTKPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRFSFSEWFGGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSVDNIGTGVAHPPRWTSdstVAEVTsiQLEfRELSRLTGDKKFQEAVEKVtQHihGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWiqGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFVGELAHGRFSakMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVtGDRKYQDWG
WEILQSFsRfTRVPsGGYSSINNvQDPQKPePRDKMESFFLGETLkYLFLLFSDDPNLLSLD
AYVFNTeAHPLPIWTPA
```

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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FIGURE 11

GCGCGCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATGTT**CCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGCTCTTCCACCTGTTCTGTGGC
 CTGCCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCGGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
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 CGGGCAGCGCTCATCAACGTGGGCTTCTTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCTCTGAGGCTGGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCATAACAAGACCTATGTCGGCGGC
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 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
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 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGTGGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
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FIGURE 14

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<subunit 1 of 1, 73 aa, 1 stop

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PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCGCGCCGGGGAAGGCCGCTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCCGCTCCTGCCGCCGGGCTCCGGGCGGCCGCTAGGCCAGTGCGCCGCC
 CTCGCCCCGAGGCCCGGCCGCGCAGC**ATG**GAGCCACCCGAGCCGCCGGGGCCGCCGCGCA
 CCGCGCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG
 GCGCGCGCGCGCGCGCTGCCCGCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC
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 GCCCCAGATACTCTGCCCAACCGCACGGTCACCTGATTCTGAGTAACAATAAGATATCCG
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 GCAATGTTTCAAATACATTTTCGAGTCTGCGCACTAAAGGTATTGTACATTCTGCAATCATTT
 AAGACTATTTCAGCT**TAA**ATTGAATGCTCCAATGTTCTGCTTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTGCGAGGAAGATAGGTATTATGCTTTTGCTACTGTTTTAAAGAAACCTA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTCGCTTTGATTCCCTTT
 CTTACATAAAAAATACAGAAATTACATTTTATACTGCAAGTGATGATGCAATGATATACT
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 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTGTGAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAGAAAAA

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FIGURE 16

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDPTLPNRTVTILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQF
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPEVVNNKGFDRWPRTL
 YLQCTRNTHSGSIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMP
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
 DERVWLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

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FIGURE 17

GCGTGGGGATGCTCTAGGAGCTCGAAGGTGGTGCTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGAAGGAGAGAGAGATGTTATTGGCAAAGGATCTCAAAAA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTGGTCACTGTCTTTTAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 18

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

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FIGURE 19

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAAACCACGACGTATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCTCGGGCCCTGACACAGCCCTGGGTCTCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTCTGTCCCACGGCCGTTCGCGGGACACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCGGCCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACAGCACAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCTCTGCTGAACCTGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGTCTGTC
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCTCTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGA CTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCAAGAGGCTCC
 CGTCCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCCTTCTCTGTTTCTCTTCTCTGTCTCCCTCCCTCCACCTTTTTCTTTCTCTCC
 CAATTCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCTCTTCTCTTCTTCT
 TTCTTCTCTGTGTTGTTTTGTTGCCACATCTCTGTTTTACCCCTGAGCTGTTTCTCTTTT
 CTTTCTTCTCTTTTTTTTTTTTTTTTTTTAAGACGGAATCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCTCTGGGTTCAAGCGATTCTCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTCTTTTTTCTCATCTCTTTTCTGGGTGCGCTGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGTGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCCTTTAAATTAATAAACATATATATATAT
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
 CCCCCTGCGACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTTGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGCTGGATGCCTTTCATCCCACTATTCT
 CTGTGGTATGAAAAAG

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FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIIACVAYATEVAWTRARPEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFEVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

[illegible]

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FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCS
LAWSFTRLRLHPPPLSPGISQVVVDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSELDGLLGSPARLASQLLGDE
LLLAKLPSPRESAFRSLGLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328**Tyrosine kinase phosphorylation site.**

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCTTGGGCGCTCTGTACACAAGCATACAGCCAGCCCCACCTAATTTGTTTCCCT
 GGCACCCTCCTGCTCAGTGCAGACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTAGTTCTGTATGTAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCTCATCTGCAAAATGGGCATAA
 TCAATCTATTCTTGGCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG
 AAGCCTACA**AATG**TGGCCTTAGCCAAAATTCTGTTGATTCAACGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
 TTAAACAAATGGAAAATAAACCTATTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACTCAAATCTCAAGGCGAGTCATTCCTCTCTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTTCTTTGGGCAGTCTAA
 AACCCACATCTACCATTTCACAAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
 TGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAGAACTCCTGATA
 ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
 ATAGTGGAAACCAAGTGAGTGGCTTACCACAAACAGTGAATAGCTTCACTGGGTTTACCCTTA
 TCAAGAAAAAACACTCTACAGCCTACCTTAAAATTCACCAATAATTCAAACCTCTTTCCAA
 ATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
 ATGACCCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**AGAA**CTAACAGCAAAAAGGCGTTAAACAGCAAGTGTATCTA
 CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTAAGTGTACAGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAAT
 TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
 TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATATTCCACCAAAAAATCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCCAGAGTTTCTGTTATTGGGAATTGAGGCAATAGAAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
 TCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGCTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHFNATPALSENFTWLSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDTSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPSEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

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FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACT**ATG**GTGAAATCGCCTTCAATACCCCTACCGCGGTGCAAAAGGAGG
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCCTTTCACTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
TCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
AATTCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTGCGAG
CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAAGTGC
TATCTGATGCCCTCAATACTTCTATTGTTATGCCCTCAAAAAATCTGGTAGAGCTCTTTGG
CAAACCTGGCGAGTGGCAGATATCGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAGGAAAAAATAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAAT
TGGCATTGCTTGTGTTTTTGAAGTGAATACATGAGTTTCATTTTTTCTTTGCATTTATAG
GGTTTAGATTTCTGAAAGCAGCATGAATATATACCTAACATCCTGACAATAAATCCATCC
GTTGTTTTTTTTGTTTGTGTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
GTGGAGCAATTTTAAATTTGAAATATTTTAAATGTTTTTGAACTTTTTGTGTAAATATA
TCAGATCTCAACATTGTTGGTTCCTTTTGTGTTTTCATTTTGTACAACCTTCTTGAATTTAGA
AATTACATCTTTGCAGTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
TTCATGAGACAGTCATTTTTAACTAATGCAGTGATCTTTCTCACTACTATCTGTATTGTGG
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA
CCCTATAATAAATTTTACTCTATACAAAAAATAAAAAAAAAA

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FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQEKEGSSGRCLMTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPKKNLVELFGKLASG
RYLPQTYVVRREDLVAVEEIRDVSNLGIFITYQLCNNRKSFRLRRRDLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCCAGAGCAGCCCCGGGCACACGACTCTCT
CTTCCAGCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCTGTACGCC
AAGGAACTGGTCTTGGGGGCACCATGCTTTTCGGCGGCAGCCCCAGCCTCTCATCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGTAGTGGGGAGGCCGAGGGCTCGTCGGCTCTCTCCCGAGCCTCC
CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTTGGGG
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGTGTATGTTTCATCGTCTGTGCCCGGTC
TCACCCGGCAGAAAGCAGAAAGGCTTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
GTGGACAGAGTGACCGGGGCGGGGGCCCCCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCGAGGAAGCCCTGGATTCTCTCCCGCAGCTCCAGGCCACATCTTGGCCG
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCATGGGCGGTGGGGACCGAGCCAGGATG
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACAGGAAGTCCA
GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGG
AGGGGGCTGTGGTGGCCGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTTTGTTAGCCAG
GAAGCCAGGGACCAAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG
TGTCTAACAGTCTCTCCGGGCTGCCAGCCCTGACTGTTCGGGCCCCCAAGTGGTCACCTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTTGACACTCCCTCCTTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGTGCCCGGA
GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
ACAGCTCCCCTGACAAAGTGAGGGAGGGCAGCTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAATACTTTTTAAACA
GCTACAGGGTAAAATCCTGCAGCACCACCTCTGGAAAATACTGCTCTTAATTTTCCCTGAAG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
TCAAGCGCTCTCCAAGCACCCTCGGCTGGGGGTGAGTTTCTCATCCCGCTACTGTGCTGG
GATCAGGTTGAATGAATGGAATCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAAGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG
CCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
TGTCACAATATTCGTAGTCTCTGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA
AAGA

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FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWPAL
SPTSMGPQPTTLGGPSPTNFLDGI VDFRQYVMLIAVVGSLAFLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

[illegible]

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FIGURE 30

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
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<MW: 42208, pI: 6.36, NX(S/T): 1
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AGSKVSEALQGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQNPGGGLTGWVHGYPGNSAGSFGM
NPQGAIPWQGGNGGPPNFGTNTQGAVAPQGYGSVVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGRFGQGVSSNMREISKEGNRLL
GGSGDNYRGQSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTGTGTCAGCGAGGGCTGCAGGCCCGCGGGCGGTGCTCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTGTCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGCAGGAGAGTAGGGGGAATGTTGTTTCTTGAACAAGC
 TGTGCTACTTGTCTTGCTGGGCTGGCTTTTCCAGATTTCCACAGTCCCTGAGGACATGTTCTTTCTGGAAGAGG
 GTCCCTCATATGCGCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCCCTGTGGTGGACCAAG
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAATCTGCTGCTTCTGGTGGTGCAGGCAGTAGTG
 GACGGAGTGGGGCTTCATGAGGAATAACCCGCCACTACCACAGCTGGGAGGCCAGCTCTCCAGACGA
 GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCCTTTTCCACAACACAGCCGCTCTCTGCGCGGACCGCTAGAGT
 TCGTGGCAGAAAGATTGGATCAAACTGTGTCAAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG
 CAGAGTCACTTCTCCAAGACAGCTGGTGACACAGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTACGGGGGCCAGGCATTTGGCCCTGGGGCGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTTGCTGTGGGGC
 TTGCAACAGAGAAGCGTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCAGGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCTGAC
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAAATTCCTATCTTAGGGCCCCGGCAGCATACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTGGAAGGAAGACTTTCAGGGGCGGTTCCGCTGCAGCTG
 CTGCTGAGCCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA
 CGGGAGCTGGTGAGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCTGCTGCTGGCAGCTCCACCGAGCCGAG
 TGCCCGAGGAGCTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGGCCCACTGCCAGCAACC
 CAGCTAAGAGCTGTGAGTTGGTGCAGCCAAACCGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGCAATGCAACAGAACCTGGACCCCGCTCAGCAGGAGGCCCAAGTGCCCAATGCAGACCCCTCAC
 TGGTTGGGGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCTTGGCATCCCAACCGCGA
 ATCCTAGAGGAAGAGAGTTGGCTGATTTGGGATTATGGCAGAAAAGTCCAGAGTCCAGAGTCCCTGGAGTAGCA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTTGGCTTGTCAACACGAATTAACGCTT
 CATTTGCTATCCCACTCTCTTAAAACTTTGTAGTCTTGAATTCATGACAGAGGCAATGACTCTGCTGTAACT
 TATAGAAAGAGTTAAACATGAATCTTGGAGTCTACATTTTCTTATCACAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCTAACACAGGCCGGGTCTGTTGGCTCATGCGCTGTAATCCCAGCTTGTAGAGGCTCAGGTCGGCG
 GACTGCTGAGGTGAGGAATCAAGACAGGCTGGCCACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCTGTTGGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCGAGGAGACTGCTTGAAC
 CTGGAGGTGGAGGTTGAGTGAGCCGAGGTGCGACCACTGCACTCAGTCTGGGTGACAGAGCGAGACTTCTAG
 AAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCTGTACTCTTCAGGCCCTG
 TGCAGGTAGTAACCTCTGAGACCTCTCCCTGACCAGGACCAAGCACAGGGCAATTAGAGCTTTTGAATAATA
 CTGGTTTTCTTTAAAAAAGGGGCTTTTATTTAAATTTCTCCCAACAGATGGCTCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTCTAGGGAAAGGCCCTGTTTCCCTGAGGCGGGGCTGGGCTGTCCATGGGTGCGCGGAGCTG
 CGCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTTCGGGGCACAGAGTGGGGGTCTGGGGGCAACCGG
 AGCTAAGACAGGCTCTGCTGACAGGGGTGGAGGCTGTCTCTTAACCGACACCTGAGGCTGCTCCTAGATGCTG
 GGTCCACCTGAGTGGCAGGGGAGCAGCTGTGGCGGTGTCTCTCTYTAGGCCAGTCCCTGGGGAACATGAGCTC
 GGGCGCTTCTTTTAAAAAAGGGGCTTGGTGGCTGAGCGGCTGAGGAGTGGGAGTGGGCTGAGGAGCTACGTG
 GAAGAGGGCGCGGCTTGTGTGGCTGCAGCGGCTGGAGCGCTCTCTCTGAGCCCTGAGTTTCCCTTCCGCTCAT
 ATGAAGACATGCGCTCTGGTCTCTCAGGCTATTAGAGCTTGGCTCAGGAAGTGGCTTGGACGAGGCTCAT
 GTTATTTTCAAACTGTCTGCGACGTTGGCTTGGCAGCTCATGGAATGGCCCATGTCCCTCTGCTGGCTGGAC
 GTGCGGCTCGGGAGTGGCAGGACAGGCGGGGCCAGAGCTGGCGCTGGGGGTGAGGGGAGGCGCCCGGAGGG
 CCTCACAGGAAGTTGGGCTCCCGCAACACAGGACAGGGCGGGCTCCCGCGCGCGCCGCCACACCGTCCAGG
 GCGCGGTGACAAAGTGAAGTGCAGCTTGGGCTGCTGCTGCGCAGAGTAGCCCTTGTGACAGTGGCGAGCGCG
 TCGTCCGCGAGCTGGAAGCAGCGCCCTCCACAGCAGCAACCGGTCGCGCT

FIGURE 32

MCFLNKLALLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLEDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQAFAFFHNQPP
SLRRTFVEFVAERIGSNCKVHKIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAGVLATEKACAWLSANITAL
IRREVKA AVSRTLRAQGP EPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGTTTTCACACAGCAGTTTCTGTCAGCTTCTCTTGAGGTGTGAACCCACATCCC
 TGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
 AGTAGCAACAAAGAGCAGCGGTCAGCAGTGTTCGTGATCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTCGGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAGAAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAGACACTGCCCTCTCGGTGCCACCACTGTGTGATTGTACAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCCTCGTGGCCCATTC
 AGTGTGTTCCGGCTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAAGCCCGAGGGCAGCCTCGTGCCTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGCATCGCG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTACCACTGCATGTCTATG
 GCATGGTCCCCCACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGACGAATGTGTCACTTACATCCAGAATGAGCACAGTCCGAAGG
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCTCGGACCTAGAGCCACCCAGCCTGTGGGACCTCAGGAGGGTCA
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTTCGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGAATTTGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTGCCAAGGAGCTGGGAATCTGGTGTG
 CCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGACAAACCCCTCCCCCTCTCTGGG
 CACCCTTCTGCCACACCACTTTCCAGTGCGGAGTCTGAGACCCCTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCGTCTGGACCCCTCCAGCCACTATCCCTTGTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAACTTTAGGGTATTTTTCG
 GCAAACCTCTCAGGTTTGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTCT
 TAGCCCCCTCAGCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTTTTCTGCCCT
 CTAGCAGGGAGGTTTTTCCAATGTTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCGAGGGTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT
 ATCACTGGGTCTGTCCCCCTGGCTCTGTATCAGGCACTTTATTAAGCTGGGCCTCAGTGG
 GGTGTGTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGACCATGAGGAGGAGGCCAGCAGCTAGCCATTGGCCTGGGTGATGGGTGG
 GGGCGGTGACTGCCCGACACTTGGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVPHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVVSSSSHLGLGPEIERAECTIRMNDAPTGTGYSADVGNKTTYRVVAH
SSVFRVLRPPQEFVNRTPETVFIFWGPPSKMQKPQGS�VRVVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPRLQRMPIYH
YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

[illegible]

FIGURE 36

MLRGTMTAWRGMREPVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMKYCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPEAQTIIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQMAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKGQAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFFIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVSYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYRPTDSDNDSYKDKMVEGDYKWHSSISHLQPETSIDIKMQCFNEGGESEFSNV
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTMAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAWKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLPPDDSTHQLLPQHHDCQREQPAAVQGSGVRRAPDSPVLEAVWDPPFHS
 PPCCGLGLVPVEVDSPDSCQVSGGDWCPQHPVGAYVQGEPGMQLSPGLVLRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAACATGACAGCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCCGGGTGTCCCAGCGCCCTACTACCCAGGCCTCACTACGCCAGG
 CACCCCAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTTCCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCTACTCTGAAGTTCGAGCTT
 GTGACCTCAGCTGAAGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGATTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAAATTTG
 TTGAATGTTCGGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTTATCCGGGATTTGGTGAAATTTATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAAGTGAAAAGGTGAGAGAGAGCAGGCGCAGAGCCCGTGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCCTCAGAATGGACACCCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGAGGTCCTCAAATGCCT
 CCCCATACCTTGTTCAGGCCCTTGTGGCTGCTGCCACCATCCCAACCTTCAACCAAGTGGCTC
 TGCTGACACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAGCCCCCTCTCCT
 AGTTCATTCACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

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FIGURE 38

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNLDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQLSTSC
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTQWLC

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Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTGTTGCTGGTGCCCCAGCTGAAGCCAAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGAGGCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCT**TAGAT**GGGCTGG
TGTGGTTGGGTCAAGGCCCAACACCATGGTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTAAAGCCTGTGGCATTTTTCTCCTT
CTCCCTAACTTTAGAAATGTTGTAATTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTCGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCAGCATTACGATGTGTTCCTTCTGCAGTG
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGGGA
AGCTGGTGTTCGCTGTCCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTCCGGTCCCCCTACCTGCACCTTGAGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG
CACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCGTACTTGGGTTGCCTCTGTCCCTGAACCTTCGTTGTACCAAGTGCATGGA
GAGAAAATTTTGCCTCTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
TTTTATTCTCTCA

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FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHHDVEAYCLLCECRYEERSTTIKVIIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGGTTGGGTTCCGCTAATTTCTGTCTGTAGGCGTGAGACTGAGTTCATAGGGTCTGGGTTCCCCGA
 ACCAGGAAGGTTTGAGGGAACACATCTGCAAGCCCCCGGACCCCAAGTGAGGGGGCCCGGTGTGGGGTCTCTCC
 TCCTTTTGCATTCCCAACCTCCCGGGCTTTGGCTTCTCTGGGACCCCTCGCCGGGAGATGCGCCCGGTTGATG
 CGGAGCAGGATTCTGCTCTGCTGCTGCTCTACTGGCCGGCGGTGCTGATGGTGGAGAGCTCAGAGATCGGCAAGT
 TCGGGGCCAAACTCAACTCCATCAAGTCCCTCTGCGGGCGGGAGACGCCCTGGTCAGGCCGCCAATCGATCTCGG
 GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGGCAAAAGACTGGGGCAGGCCTACCCCTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCCAAGGATCATCGGCTGCATGGTGTGTCGGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCAAGTACCCGCTGCAATATGGCATCTGTATCCCAAGT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAACGGTCAATTAC
 TCAAAACCATGACTTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTGCATATATAAAGGGGATGAAGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCGGACCAAAATCTGCAAA
 CCAGTGTCTCCATCAGGGGGGAAGTCTGTACCAAAACACGCAAGAAGGGTCTCATGGGCTGGAAATTTTCCAGCGT
 TGGCACTGTGCGAAGGGCCTGTCTTGCAAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTTCAGATGCAGAAGAAATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAAGAAAACATGAACCTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCCTATTATG
 CAACTTGTCTATGTAATAATGTACACATTGTGGAAAATGCTATTATTAAGAGAACAGACACAGCTGGAAATTT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATCCGAGATTCTATTCAACGTTAGAGTTTAAACAAAATACTCCTAGAAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATTTGCTAAACAGAAATGAAAACATGGAGCAATTGTTAATTTACACAGAAAAAT
 TACCTTTTGTATTGTAAACACTACTCTGCTGTTCATCAAGAGCTCTTGATAGATAAGAAAAAATCAGTCAATAT
 TTTCCAAATAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCCCTTAGGAAGCAAAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGCTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCAA
 AACTATACCCATAAATTTGTGACTAGTAAAAATCTTACACAGAGCAGAAATTTTCAGATGGCAAAAAAATTTTAAA
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATATTTCCTTAAAGATTGGCCATCAACCTATATTTT
 GATAGAATTAGATTGGTAATACATGTATTCATACATACTCTGTGGTAATAGAGCTTAAGCTGGATCTGTAAGT
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGCTGT
 AGGCACAAGTTGGCTGTTCACTCTTTGAAACCAGGGGATGCACAGTCTAAATAGATCTTCGATGGGATTGTCTAT
 CATATATTTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCGCTACTATCCTCAAAATTTATTTATTTATAG
 TGCTGAGATCCTCAAAATAATCTCAATTTGAGGAGGTTTCAAAAATGTACTCTCTGAAGTAGACAGAGTAGTGAGG
 TTTCTATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTCTTCCCAAGCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAATAAAGTAGGATAACTTTGTAAA
 ACCTGCATATTTGCTAATCTATAGACACCACAGTTTCAAATCTTTTGAACCACTTTACTACTTTTTTTTAAACTT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACATAAAAGGTTATCTTATAGCTGTGACTTTAAACTTTTG
 TAGACCACAACTCACTTTTATGTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAAATTTAAGTTCTCCCGTAGT
 AGATTGAGTTTGAGCCTGTATCTATTAAAAATTTCACTTCCACATATATTACTTAAGATGATTAAGACTTA
 CATTTTCTGCACAGGTCGCAAAAACAAAATTTATAAAGTCTGATCCATCCAAAGCAAAAGTTTGTATAAACAGGT
 TGCTATAAGGTTGTAAATGAAATGGAAACATTCAATCAAAACATTTCTATATAAACAATTTATTTATTTTACAAT
 TTGGTTTCTGCAATATTTTCTTATGTGCCACCTTTTAAAAAATTTATTTTGAAGTAATTTATTTACAGGAATG
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGAGCAGAAATATTTTGCAGCTATTGAC
 TTTGTAATTTAGGAAAAATGTATAAAGATAAAATCTATTAAATTTTCTCCTCTAAAAAAGTAAAAAATAA
 AAAAAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGNLGOAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCEN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA
GTGTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
TCTTCAAATTATGGCAAATATTTCCTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGA
TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTGTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACACTACTTCTTGGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCATGTTCTCTCT
CCTGGTTTGGAGTTCCTTTCCTTCCCAGGCCAAAACCTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGCAGCTTCCAGCAGCAGCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCGAGCTTCTAAG
ATCCCGAGTCTCTGCAGTGGAATGCCTGGTTCAGCAGATGTACAGGATTAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAGTGCACTACAGAACTCCACATATACAACCTTCCGTCAATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTTCTGCTAGTCCAGTAGCAATGTCTTCTCTTTATGACC
AGAGTCTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
GGAACCATCATGAATGGACATGGTGGTGGTTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTGTGCATGGCTGGTGCCAAACCAAAGAGGAGGATAGCTCAGCTGA
TGTGGAACCAACAGTGGTCAATGGCTCATTGCT**TAA**AAAGCAGCCCTTTTGCTTTTGTG
TTTTGGACCAGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCAAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAATC
TGCTCTACTAAATACGAAAAACTAGCCGGGTGGTGGCGGCGCGTGCCTGTAATCCAG
CTACTTGGGAGGCTGAGGCACAAGAAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAA

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FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQFPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGCGCTGCCATCCCCGAATCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCGCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCGCGCTCTTCCACCTGACGGTCGCGGAACCCACGC
 GGAGCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCAG
 ACCCCACACTGGGCGCGGCCACAACGTATCAATGTCTATCGTCCCCGAGAGCCGAGCCCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGCTCAC
 TGTCTCTGCGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCTCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAACT
 GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCTCCAGGGCTCTGCTGCTCCGGGCTGGGAGATGTTCTTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGTCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTTGCCTTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAAATAAGTCCCATCTGATTTTTAAAAA
 AAAAA

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FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGD FSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPIRGSPNGSSSHSGAPGPDPTLARGHNVINVIVESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKGDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

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FIGURE 47

CGCCGGAGGCAGCGGGCGCTGGCGCAGCGCGAC**ATGGCCGTGTGCTCAGAGGACGACTTT**
 CAGCACAGTTCAAACCTCCACCTACGGAAACCAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTACGCTGGGCATTGGCAGTCTACTGCCATGGAACCTTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCAGCCACCGGGGA
 GGACCTTGAGGGCTCAGACATCTTGAACCTACTTTGAGAGTACCTTGCCCTTGCTCCACCG
 TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGCTCTGGCCTCACTGACGGTCATCTTGCCATCTTATGGTGATAACTGCATGGTGAA
 GGTGGACACTTCTCTGGACCCGTGGTTTTTTTGGCGGTACCATTTGTCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGACGCTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTTGCGGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTCATTGATTCCACACACCCCTCTCC
 GCCCCCTCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCAC
 AGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCCTCTGTACAACCTTTGCTGACCTAT
 GTGGCCGGCAGCTCACCCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGCGCTCCCAGGG
 TTCGTGCTCCTCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAAGCCCGCT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCCTCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGCCCTAAGATTGTGCCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGCTCTTTATGTGTGCTTTGGGCTTAACACTGGG
 CTCAGCCTGCTACCCCTCCTGGTGACCTCATC**TAGA**AGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCAGTCAATTAACAGAACT
 CCTGAGACAGTTGAAGAAGAAATAGCAAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTCCACCTTTCTTTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
 AAGCAGTGGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGCGATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAACAACCTGCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCCTTCCATGAAT
 GCTTCATTCCAGAGGGACAGAGGGCTCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
 GTATTCAAAA

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FIGURE 48

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPFGLQRPEDRFCGTYIIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLA SLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
TCTCCACCAGAGATCAATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCAGAAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCGAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
CGATGAAGAAGTTTGAAGGCACACGCTCTTGGAATATCTTCTCGGGAGGGGAACCTGAGC
CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGTGTCCGGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATCACCTTCTCGCCGCCGTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
CTGCACTACGTGCCGCCACCAAGGTGTTCTTAAGCTTCCGACGGCCCTTCTGGCGCGAGGA
GCACATTGAAGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCGAGCGTTGCGC
GGCTTGAGCCGGGAAGAGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTGTCAAGCGTTGGGCGGAGGACAGCACACA
GCCAGGTGGCTTTGTGGTACAGCCGCCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTTGCCGCGGAGCACACCGCCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
CGGACACGGCCAGCCCCAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG
CCAGTTATCTCTCCAAAACACGACCACACGAGGACCTCGCATAAAAGTATTTTCGGAAAAA
AAA

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FIGURE 50

MAPLALHLLVLVPILLSLVLASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
 IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIIL
 HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLGALRPQEKGHSPEDIYQMA
 LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDEGFFYLSFAEALR
 AHSCLSDRLQYSRIVGGWDLPLRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
 KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPFWREEHIEGG
 HSNTDRPSRMIFYPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPPVVRQL
 WDGTVVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
 ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGGQLSLQ
 NTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GGACGCTCTGAAGCCACCTGTCTCTGGAGGAACACAGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACCTCAGAGCGGGGAAGCGCCCATTCAGTGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCCCT
 GCTGCTGTTTCAAAAGATGCTTTTATCTTTAACTTTTGTGTTTCCCCACTTCGACCCCGGGCTGTATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTTTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGACGACGGAAGGGGGTTTCCAGAGAACAATGACCTAACAAGTTGCTG
 CTCTCAGATGCCAAGACTGATGATGAGGTTTCCAAAGAGGACTCGCTGTGTGACAAATGGGCCCTGCTTGGG
 ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAACAGGTGTCTGATAGACAGAGTACCTGGGTTTC
 CTGCTCTTGCATAAAGGTTATAAATCATCACCAGACCAGTTTGTGGCATCTTTGCTCAGATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACCAGAAGC
 CATCGTACATATTGTCAACAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATTTGGTCTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCAGGCTGAAGGTGATCATCCTTATGACCCCTTTTGTATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCAAAGAGCACTTCAG
 AAAACCTGTGCCTCCTAGCCAGAAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAATATTTGTTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGAGGATGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCAAAGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTTCCCGCGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTAACAATGAGGCCAAGACACCTTT
 GAAGAAGTTCTTGTTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTTCTGGGACAAGCTCATCTTTCAAAGATCCAGGACAGCCTTGGCGGGAAGGGTTCGTGTAATTTGCACTGGAGC
 TGCCCCCATGTCCACTTCAGTCATGACATCTTCCGGGCAGCAATGGGATTCAGGTGTATGAAGCTTATGGTCA
 AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTCACTTTGGGGTCCCTTGGC
 TTGCAATTAAGTGAAGTGGAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGCTGCAT
 CAAGGTCACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTCACACAGGAGACATTGGTGCCTGCCGAATGGAATCTGGAAGTCAATGCAACATAAAGAACTTT
 CAAGCTGGCCCAAGGAGAAATACATTGCACAGAGAAGTAGAAAATATCTACAACAGGAGTCAACAGTGTATACA
 AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTCTTGACACAGATGTACTTCCCTC
 ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACCTGTGCCAAACCAAGTTGTAAAGGGAAGCCATTT
 AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAAACCTTTTGAACAGCTTAAAGCAATTTTCCCTC
 AGAGCCATTTTCCATTGAAAATGGGCTCTGACACCAACATTTGAAAGCAAGAGGAGAGAGCTTCCAAATACTT
 TCGGACCCAAATGACAGCCTGTATGAGCACATCCAGGAT**TAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG**
 TGCACTGCTTGTGAGAAAATGATTAAAACTATCTTACATTTGTTTTGCCTTTCCCTCCTATTTTTTTTAACT
 TGTTAAACTCTAAAGCCATAGCTTTTGTTTATATTGAGACATATAATGTGTAACCTAGTTCCCAAATAAATCA
 ATCCTGCTTTCCCATCTCTGATGTGTGCTAATATTAAAGCTTCAGGGCTACTTTTATCAACATGCCCTGCTTCAA
 GATCCAGTTTGTGCTGTGCTTCTCATGATTTCAACCTTAACTATTAGTAACCAACAGTTTCAAGGCTCTT
 CAAAGGGACCTCTGTGCCCTTCTCTTTGTTTGTGATAAACATAACTTCCCAACAGTCTCTATGCTTTATTACA
 TCTTCTACTGTTCAAACCTAAGATTTTTAAATCTGAAAAACCTGTACCAATCTATGTTCTTAGCCACTCCAC
 AAACCACTAAAATTTAGTTTATAGCCTATCACTCATGTCAATCATATCTATGAGACAATGCTCCGATGCTCTT
 CTGGCTGATTAATTTGTGTACTGAAGGGAAGTTTGATCATACCAACACTTCTCAACTCTCTAGTAGATA
 TCTGACTTGGGAGATTTAAAATTTGGGCTATGACATCTGTCCAAAGGAATGCTGTTCTTAAGACATTAATTA
 CAGTAGGAGACTGGGGAGTAAATCTGTTCCCTACAGTTTGTCTGAGCTGGAAGCTGTGGGGAGGAGTAGCA
 GGTGGGCGCACTGAACTTTTCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGTGACTTGGGAACAAGATCT
 ACAGCAAGCAAGATGCCACAACAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCCACTTGGATT
 AGAGTTCTCTGCTTACCTTACCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC
 TATTACAGATAAAAAA

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FIGURE 52

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
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CCFSDAKTMYEVFORGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCVEHAYEPTPDDVAISYPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMDKTLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVIVTGAAPMSTSVMFTFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPPLACNYVKLEDVADMNYFTVNNEGEVCICKTINVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEFFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD
```

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCGGGGGCCCTAAGCCATTCTCGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAAGTACAAACAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGGCCGTGCTTTTCTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGCGATCCATGTCTATTGCTTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGCTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTCTATCCT
 CAACATGGTAGCGCCCGCCGAGTGCTCATGTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGGCCTTCGTGGGACGAAAAGAGGTCCTGTCTTCGGGGAGAAACATTTC
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAAGGCGAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTCTCAGCAAAAGTTGAGGGCTATGGAAGTGATGCACTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGTCTCAATGTGCGCTGTGGCTGCTATTGCGAG
 GGAACCGACCCAAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTACGCCAGGGGGTGCTG
 CTCAGATGATAACAGTTTCTATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTTGGTCTGAGGGGACATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCTGTCTCAGC
 ACTCAAGGCCAGCGCTCACTGCGCACTTTCAACCTGTTCCGGAGGCCAAGTTTGCTGTGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCTCGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTTGGAAATGACAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCTTGGCTGGCTGGGTGCTC
 AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCAAAGTGGCTTACACCGGAAAGCTCTGGGA
 TTGGGCATGTGGATGCGGATGCGCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGAGC
 TTTCCCGATCCTACCCTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCACAGGTGTCCAGCTCAGGAATGTGGACAGCT
 GAAGAAAGAAGCTTATGAAGTGAAGTTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGAGCC
 ACAGCAAGAACCCTTGTGAAGACTCTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGGAATGGAGAAAGATGATGACTTCACACCTGGACCCAGCTTGCCAAGTGCCCTCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGTGTGGTGGGGGCTCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCTCAGTC
 ACCCCAATTTTCTGGAGCCACCCCAAAGGAGGAGGGAGCGCCAGGAGCCCAAGAACAGAC
ATGAGACCTCCTCCAGGACCTGCGGGGCTGGGTACTGTGTACCCCAAGGCTGGCTAGCCCT
 TCCTTCATCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA
 TGAGACTTAATTACTAACTCCAAGGGGAGGTTTCCCTGCTCCAACACCCCGTTCTGAGTT
 AAAAGTCTATTTATTACTTCTTGTGGAGAGGGCAGGAGATACCTGGGAATCAATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCTTGCTCAGAATCTA
 ACCATATTATTGACTGTCCTGAGGGCCTTGAAACAGGCCGAACCTGGAGGGCCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCATGGACAGGCCCTAGCTGGGGCCACATGCTGACACAGACTACTCAGAGACCCCTTA
 GACACTGGACCAGGCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
 GTTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAAGCTGGAAGGCCACTCTCTTGGAAACCACCACAC
CTGTTTAAAGAACATAAGCACCATTAAAGCCACTGGAATTTGTTGTCTAGTGGTTGTGGGTGAATA
AAGGAGGGCAGAATGGATGATTTCATCTCCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA
CGTGGCCGGAATCATTCCCTTGCTGTTAATTTCTCAGAGGAACGACATGAAGCTGGTGACTGTTTGG
GTGCTGGCCCTTCTCTGTGGAATCTGCTTGGCAGTCATCGTGCCCTGAAGGAGTACATGCCCTTTATGAA
GTATTCTTTGAGGGAAAAACACCACCAAGCAAGTGAACACACATAATGTGATTGCATCAGACAAAGCAGC
AGAAAAATCAGTTGTCATGAACATGAGCAGCAGCCACGACCACACACAGCTGCATGCCATATATTGGTG
TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAAGTGGTAACTCCCATGGTGCATCTCT
ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACACGCTGGGTCTGGTTGTCCA
TGCTGCACTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTACAGACCAAGTGTCCAGTTAATTG
TGTTTGTGGCAATCATGCTACATAAGCACCAGCTGCTTTTGGACTGGTTTCTTCTGATGCATGCT
GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCAT
GGTGACATACCTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTTAGAGGTGAACGCCACCGGAGTGG
CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGAGGCCCTCAGCCGCTGGAAAGTGGCAGCCCT
GGTCTGGGTTGCCCTCATCCCTCTCATCCTGTCACTAGGACACCAAGTAAATGTTCAAGGTCCAGC
CTTGGTCCAGGGCCGTTTGCCATCTCAGTGAGAACAGCCGGCAGCTGACAGCTACTCACTTCTCTCAGC
TCTTGTCTCACTTGGCAGTCCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTAAAAACCTG
AGTAATGGAAAGCTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTTG
TATCTTTTAAAGGCCCTTGACATTTTGGCTTTTAAATTTCTCTTAACCCCTATTCTCAGGGAAGATG
GAATTTAGTTTAAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATATGAAATACAGT
GTTCTGTAATTAAGCTATGTCCTTTCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTT
AACATGGTTCACCATGTGAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCTATA
GCACCACTCATTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGCTCAGGAAAAATGATAGC
AAGACACATTGAAAGCTCTCTTTATCTCAAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT
TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAATGAGCAGGAGG
TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAAT
ACCTGTCTCCACATCTCTAGAGAGGAGCCAGTTCTAGTAGTTTCAGTTCTAGGCTTCTCTCAAGAA
CAGTCAGATCACAAGAGTGCTTTGGAAATTAAGGGATATTAAATTTTAAAGTGATTTTGGATGGTTAT
TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTTTGT
TTTTTTTTTAATTAATTTCTTTAGCAGATCAGCAATCCCTCAGGGCAATAATACCTAGGTCAGCTTT
GGCGACACTGTGCTTCTCACATAACCACCTGTAGCAGATGGATCATAATGAGAAGTGTTTGCCATA
TTGATTTAAAGCTATTGGAATCATGTCTCTTGCTCTCTCGTCTTTTCTTGGCTTTTCTTCTTAACCTT
TCCCTCTAGGCTCTCTCGGCCACAAATTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATT
CTTATCAGGACAACCACTCTCGAACTGTAATAATGAAGATAATAATCTTTATCTTTATCTCCCTT
CAAGAAATTAACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCTCATGTGTAA
ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA
ATTTTTTTTTCATATTTGCCAAAAATTTTGTAAACCTGTCTGTCAAAATAGTGTAATAATATTGTAT
TATTAATTTATTTTACTTTCTATACCATTTCAAAACACATTAACATTAAGGGGGAACCAAGACTAGTT
TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACAGTTTTCTATGACGCATAAGCTAGCATGCCATATG
ATTTATTTCTCTCATGAATTTGCTACTGGATCAGCAGCTGTGGAAATTAAGCTTGTGAGCCCTCTGCT
GGCCAGTGGAGGAAGTAGCAAAATAGGATACAGTTGTATGATTCATTGGCAACAAATGGATACA
ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCTTGTATTGGATGTTAAACAGCT
GACTGGTGTGAGACTTGGGTTTCTATCTAGTCCTTCAAACTATATGGTTGGCTAGATTCTCTCTGGA
AACTGACTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAA

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FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGTFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTTGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGCGGAGAGCGACCCGGGCGGCTCGTAGCGGGGCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTGGTGAA
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCGTCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA
 TGAGGGGCCCTGAGCGAGACCAGCTTGTCATCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACACGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
 VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
 KTLQRNYGRLLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
 SRDLSENNDQRQQLQALSEPQPRQAAGLPHTVEVPQGKGNVLGNSKSQTPAPSSSEVVLDSCR
 QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
 ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
 RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCGAAGAAGCCTCAGTGTGGCTCTTCCTGGGCTGGGTCTGCTTCTCTTCTACGCTGGCATTTGCCCTCTTCA
 CCGATGGCTTCTCTGCTCACCCTTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGGCATGGGGGAGCCAAAGGGAAACCTGGGGCTGCTGGATGGCTTCCCGATTTCGCGGGTTGGTTGGTGCTGA
 TAGATGCTCTCGATTTGACTTCGCCAGCCCCAGCATTCACACGTGCTAGAGAGCCTCCTGTCTCCCTACCCCT
 TCCTGGGCAAACTAAGCTCCTTGCAGAGGATCCTGGAGATTACGCCCCACCATGCCCCGCTCTACCGATCTCAGG
 TCGACCCCTCTACCAACCACCATGCAGCGCCTCAAGGCCCTCACCAGTGGCTCAGCTGCCCTACCTTTATTGATGCTG
 GTAGTAATCTCCGAGCGACCCCATGTGGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGAGGGCGTGTAG
 TCTTCATGGGAGATGATACCTGGAAGACCTTTTCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA
 ATGTGACAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTTACCCCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGGCCCTCACCACCTGAAATGGCCCA
 AGAAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTTGGAGATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCAGCACCCACAGAGGACGAGGTGATTCTCAAGTTAGCCTTTGTGC
 CCACGCTGGCCCTGCTGCTGGGCTGCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGGCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCGCATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCCATGTGA
 TTGCTGAGCTCGACAGTGTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTCTCTCTCTGGTCC
 GCATGGCGGGGGTACTGCTCTCTGGCTGCTTCTGCTTTATCTGCTCTGAGCTCAGTGAGGCAATATCC
 CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCTCGGGGCTGGTTGGGGCCATAGCGTATCTGGAG
 TCTCTGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGACAGTACTATCTCTCCCTT
 TTCTGTGGAAGCCTGGGCTGGCTGGGGTCCAAAGAGGCCCTGGCAACCTGTTTCCATCCCTGGGCCCCGTCC
 TGTATTCTCTGCTCATTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTGAGCTGAGGCGAGGCCACCCCTT
 TCTTTTGGGCTACTTCATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACTTAAGCTAC
 TCACAAATGCCCGCTTGGCAGCTCAGGCCACAACACCCCAAGGCGCAATGGTGATATGGCAAGAGCTGTGG
 GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAAGAGACACCTGTTGCCACT
 CCTCTCCCTGGCTGAGTCTCTGCGATCCATGGTGGTGGTCGAGCCAAGAAATTTATGGTATGGAGCTTGTCTGG
 CGGCGCTGGTGGCCCTGTAGCTGCCGTGCGCTGTGTGGCTTCGCGCTATGGTATCTCAAGAGCCCCAGGCCAC
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATGGGTACTGCTGCCATCGGCACTGGGCACTGGCCTCGGG
 CAGATGAGGCTCCCCCGCTCTCCGGTCTGCTGCTGGGCGATCATGGTCTGCTCTGGGCTGTAGCAGGGC
 TGGCTGCTTCAGGGCTCGCGCTGCTCTGGAAGCCTGTGACAGTCTGGTGAAGCTGGGGCAGGCGCTCCAA
 GGACAGGACTGTCTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGTCCTCTGCT
 TCTACCGACACATGCAGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAAACTCAGGGTCCCCGACTGTGGCT
 CTTATCAGTTGGGAGTGCTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGGCTTCCACTTCTGCTGT
 TGCATCGGGAGGAGTGCATCTGTTGTTCTGCTTCTGTTTCTGAGAGTCAAGGGCTGCGGAAGGACAGCAGC
 CAGAGGGTATGGCTCCTGACTTGGCTGCTGCTTCTGCTGAGATCAAGGGCTGCGGAAGGACAGCAGC
 CCCCAGGGAATGAAGCTGATGCCAGAGTACAGCCGAGGAGGAAAGAGGAGCCACTGTGAGATGCGGCTCCGG
 ATGCGCTCAGCACTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACCTCTTATCTTGGTATTAGATTT
 TGGCTGTGCTTGGCAGCTCCATCTCTCGCAGGCATCTAGTCTGGAAGTGTTTGGCCCTTAAGTTTCATAT
 TTGAGGCTGCTGATTTGGATGATCTGTGAGCAGCGTGGGACTTCTGGGCAATGCTTGGTGATGAGATGATGGT
 CTGTGAGCTCTGGTTACGGAGCTATTTCTGGCCAGCAGAGTAGCTAGTCTGTGATTACTGSCACTTGGCT
 ACAGAGACTCTGGGAACAGTGTAGCTGGCTGTACAGTACTGGATGCTGAAGCAGGCTCAGGCATAC
 TCTTACTATCATCAGCAGGGGGCGCTGACATCTAGGACTTCAATTATCTATATCTCAGGACAGCTGGAGTA
 TGATCCCTAACTCTGATTGGATGATCTGAGGACAGGGGGCGCTCCGAGTGGGAATAAATATAGGCCCG
 GCGTGGTGACTGCACCTATAATCCAGCACTTTGGGAGGAGAGTGGGAGGATTGCTTGGTCCGAGGATCTGA
 AGACAGCCTGTGGAACATAACAAGCCCCGTCTACTATTTAAAAAAGGTGAATAAATGATAATAT

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FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
 MASRFSRVVLVLIDALRFDAQPQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
 VDPPTTMMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
 PGAFSKAFFFPSENVRLDLDVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHP
 AKKLSQMDQVIQGLVERLENDTLLVVGADHGMTTNGDHGGDSELEVSAAFLYSPTAVFPST
 PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
 QVSRFLHTYSAAQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGPFPCPLLLTPVAVGLVGAIA
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLFR
 LAAVFFSDSFVVAEARATPFLGGSFILLVVLHWEGLLPKLLTMPRLGTSATNPPRHNGAY
 ALRLGIGILLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA
 AVRLLWLRRYGNLKSPEPPMLFVRWGLFLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHM
 QEFGRRLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQSFL
 LLHLLAAGIPVTTGPGFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAVFGFPEGHGS
 CTWLPALLVGANTFASHLLFAVGCPLLLWPFCLCESQGLRKRQPPGNEADARVRPEEEEEEP
 LMEMRLRDAPQHFFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWKVFAPKFI
 FEAVGVIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAAACATCACCTTCTTATCCATCAACATGAAGA**AATGT**
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTGT
 CCTGACAGTCCAGAGAAGTGGAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 GTTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCGAG
 AGGAGGTGTCCACACAAGGAACATTATTTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
 AAACCTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGCG
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTATGGAGGAATGGGGGT
 TATATGTGCAGATGGAAACT**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815  
<subunit 1 of 1, 442 aa, 1 stop  
<MW: 49932, pI: 4.55, NX(S/T): 5  
MSYNGLHQRVFKELKLLTLCSSSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNFED  
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYDYDVRTTDICAGPEEQELSL  
QEEVSTQGTLLSQAAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCPESEGDGLGEEGLLSRLYEAPADRRPPGENETYLMQFMEEW  
GLYVQMEN
```

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

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FIGURE 63

CGGACGCGTGCGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCGAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTCGAGGA
ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCGGCC**TGA**GCCACAACCT
TGCGGCATGCAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCLTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCGTGACGCCTGA
CGCCTGTCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
AAGTGAAAGCCTCAGCCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCCATTGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT
GCCAGAGCAAGCTCGCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAAGTACTTCGATGGACTCAAACAGAAAGCCCCGGCCCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGTTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCCTCCAGATTAACCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCACTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCGCAGCTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCTGTGGGACCT
TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGCACTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCC
GAGTTACAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC
TTGCTCATT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVFNARHLDLASLKSIREFAAKIIIEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELG RHTGIHGSTF
SSTTLGP IFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQFLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATGT**GGTCCTGGGCGCGGGCTGGCGGCGCTGCTGGCGGTGCTG
 CGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCGGCTGCTGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTGATTCTACGACAAGTACTTTCTTTGCTAT
 GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCATTTACTCTCATCAACCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATCGGGCTCGAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCAACGGCTCTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGACAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTTGGTAGC
 TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAAGCCCTGGGTCTCCAGGCCACTCTCTACAGATCCCTAGCCTCTACTGTTCTTAT
 GAGACCAATTCCAACGCCTACTGTGCTCCAGCCATCCGGAAGGAGGTATCCACCTGGA
 GCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCTTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCTCAA
 CCACCGCATTGCTGCCCTCAGAGCCCTTGATGTCCGGCCTCCCTACAGAGTATCTGTCAG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTGCCCTGTGGTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAAT
 GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAAACAAGTGATATACATGATATGG
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGGAAGAAGGCCCTTGTCAGCTTTGCTGTGCTCGCAAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCCAGTACAAAGGAGGGGGGAGTGGAGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTCGATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATAGGACACCTGCAGGAG
 GGCCTAGCCTGACTCCCAAGACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGGCCAAG
 CAGGGAGTGTCCCCCTCCCAAGACATATCCAGATGAGTGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTA
 ATGTTTATAATCAAAA

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FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHVSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIEYQGFEFRPCSSSPED

Signal peptide:

amino acids 1-19

GAGATAGGGAGTCTGGGTTTAAGTTCTCTGCTCCATCTCAGGAGCCCCCTGCTCCACCCCTTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAAACCCGCGCGGGGAG
CGCCAGG**CATG**CCGCGCGGGGACTCGGAGAGGTTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCTCATCTCCTCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGCACAACTGTACCTTCTCAAGACTTATCATGTACATCTTGGGAT
CTGCTCATCATGGAGGATCATTTGGTGGCGTGGTGGCCCTTGACCTTCGGAAACAGACCATTG
ACTTCTGAAACGACAACATTGGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
CCTGTGTCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC
AAGGAGCGTTTCAAGTGTGCAGGATGTCATCTACGTGCGGGGTGCACCAAGCCGTGATCAT
CTGGTTTCATGGACAACACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCAAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCTGGGCGCCCGGTGCCAAGCCACGCGTGGAGGCGGCAGGCACGGG
ATGTCTGCTTGTGCTACCCCAAT**TAGG**CGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACTCTCAGTCAACATCTGTGGCGGTGGACAGGCGTGGCGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTTCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCGCTCCCTTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCACCTGGGCGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACTGTAAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
GTTTTTTTACGTGATTTTTGTAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCGCATGTCTATTCTTGTGCCCTCCCCAACAGTGTGTTAA
TCAAACAATAAAAAACATGTTTTGTTTTTTTAAAAAAA

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLIISTVFVWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLA SLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGGCCGGCCCGTGACCTTCACCCCTTCTCTGTGGTTTGTCTGCGAGCCACC
 TTGATCCAAGCCACCCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAATGCTGTATAAGCTCTCCTTCTGGTGAACGCCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGACCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCTGAGATCATCC
 ACTCCATCCTGTGCCGAACCAAGATGGCAAATTAAGATCTGGGGTCCCACTGTCTATTGGTG
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop .
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGFWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQAATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVKTFWNNSAASLTMTPLDNIFFSLIVSQDVVKAAVAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTASLWKPPSPVVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATTGGTGGTGGCGCTG
 CTCATCGTTTGGCAGCTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAGACCTGTAATAAGAAATGAATGGAGACA
 AGTTCGCTGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTGCTTGGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAATCCTTGGCGATACCTCCAGTGCATTACCAACACAGGATATTTTTGCCATGGTGGATTGG
 ATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTAGCTCCAACCTTTCATCAACTTT
 CTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAAGCTGATGTCAATATTAGAGTGATTAGAGCCCC
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTCAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAAGTTTGT
 GCTGAAACACACATTGTTCTTCTGTTTAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTTCTCAGTTGGATGCTCTCTATTTTATAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCCTTTTTTTCAAGTGATTAAATAGTTAATCATTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAAATAATTATCCTCTTAACTTCTCTT
 CCAAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTAAAAAATTTAAAA
 CTACTACTTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCCTTATCCAAAGATGGGGAAGTAAGTCTTGACCAGGTGTTCCACATATGCC
 TGTTACGATAACTACATTAGGAATTCATTCTTAGCTTCTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCACTTTTCTTTTGTAGTAGAGAAATTATGTGTGTCATGTGGTCTCTGAAATG
 GAACACCATTTCTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTAGATTTCATTCATCTCCTTAGTTTTCTTTAAGGTGACCATCTGTGATAAAAAATA
 TAGTCTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
 TTGTCACCTATTCCATTTGTACTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGGCAGTGACTTACGCCGTGAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCTTGCCCAACATGGTGAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAACTCACTTGAACCTCAGGAGATGGAGGTTTCACTGAGCCGAGATCAGCCACTGCACTCC
 AGCCTGGCAACAGAGCGGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWNTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLA VIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCGC**ATG**CTA
 CTGCTGTGGGTGTCGGTGGTCGACGCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGGTGGTGGAGCGACTCCTTCGATG
 GAAGGTTAAACATTTTCATCCAGGAAGTCAGGTAGTGAACCTTCCTTTTATCAACTTTTATGAAG
 ACAGTGGGACTTCCTTTCTGAATGCCTACACAAACTCTCCAATTTGTTGCCCATCACGCGC
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAAATAATTTTAAGGGTCTAG
 ATCCAAATTATACAAATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCTGTGGAGCGTGGACAAG
 AGATGTTGCTTTTCTTACTCAGACAAAGAGGAGGCCCATGGTTAATCTTATCCGTAACAGGA
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATTACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTTACTTGGGATTAAATTTACCACACCC
 TTACCCTTCACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTTCACACATCTCTTTAT
 GGCTTGAAAAAGTGTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTGAGAAATG
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAACTGCATGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGGCTGGTG
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTTCAGAAAATATTGTGCATATACTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCGGCCACAAAGTATCAAAATG
 TGGTTTCTCTTGTGGATATTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATCTTTGTTGCCCTTATCATCAGAAACATTTAAGAATGAACATAAAGT
 CAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGGCTCCCA
 CCTACATGCTTCGAACTAACCACTGGAAATATATAGCCTATTCCGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTTCCCGGATCCAGATGAATTAACAAATGTGGCTGTAATAATTTCC
 AGAAATTACTTTATCTTTGGATCAGAAGCTTCATTCCATATAAACTACCCTAAAGTTTCTG
 CTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAACAAAGTATAGGACAGAAAT
 TATTCAAACGTTATAGCAAACTCTTAGGTGGCACCAAGACTGGCAGGAAGCAAGGAAGTA
 TGAATAATGCAATTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA
 GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
 AAATGAACACAGTTTTAATAATTACCAAGTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAGGTCAAGAGATTGAGACCATCTCTGGC
 CAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGCCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCG
 AAAAAATAAAAAATAAATAATAATAATTACCAATTTTTATTATTTTGAAGAATGTAGTG
 TATTTTAAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGGTTATTATTTA
 GGCCCTTTGACAAATTTTCAACAAATTAGTGGAAGTATCAAAAGGATTGAAGCAAACTGTA
 ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAAT
 AGTTGTATGTGAGCATTTGATGGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLKVKSHDAIKIPKWSPLS
EMHPVDYYSSTYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVII
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSVLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV
```

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACTTGTGGGTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCAGCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCCGAGCCAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTTCATTCCTGTGTGCCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCTGCCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCACCTAATCACATCCCACTG
 ACTGACCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATGTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIAQAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIPAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 79

GCCTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTGAGAAAGACATAGAAAGAAAATCAACTTTCACATAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCTT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

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FIGURE 82

MAPRGCIVAVFAIFCISRLCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCCGCCGGCCGCTCCCGCCCGCTCCCGGCACACAGAAGTTCCTCT
 GCGCGTCCGACGGCGACATGGGCGCTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGCGCAGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGGAGGTGCAGACCTGCTCAGAGCGCCGCCCATCCGCAACCTACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCCTCCTCCAGGATAGTGAAAACATCAGGGTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGGCTCCCCCTCATCTGCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCGCTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
 CCCCTGTCTCCTCCAGGCCCCGAGACGTCTTCTCCCATCCCTGGACCCTGTCCCTGACT
 CTCCAAACTTTGAGGTATCTTAGCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCTTGGCTCCCCCGTTTGCCCGAGGCTGCTCTTCTGTG
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGAAG
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGAGGTGGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCACTCCCCTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCACCCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTA AAAA ACTACATGGGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPDVK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQAASNNRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFVPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTTGCCCTCC
 TTTCTTGCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCTCCCCGA
 CTCCGCTCCCGACCGAGCGGCCTGACCTGGGGAAGGATGGTCCCGAGGTGAGGGTCTC
 TCCTCCTTGCTGGGACTCGCGTGCTGTGGTTCCTTGGACTCCACGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGGTGGCACCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACC GCCTCCACTGTCGCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCTTGCC
 AGCACAACGGGACCATGTACCAACAGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCAAGTGTGTCTCTGACGTGCACAGAGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGACGTGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGG
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCGGTGCCCTTCGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCGCTCACCCGAGAAAAGTGGCTGGGAAGTGCTGCAAGATTGCCCCAGAGGACAAA
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHYPYLPQGLMYCLRCT
CSEGAHVSCYRLHCFPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSD EED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDS DQESQEARLPERGTALPTARWP PRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

[illegible]

[illegible]

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FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDGTYISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQ
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
CCGTACCTCTCCTGTCACTCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTGTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCACTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
GATAGAGACATCCAGCTACTCTGTCTCAGTCTCGGGCTGGTTCCCCGGGCCACAGCGAAGTG
GAAAGGTCACCAAGGACAGGATTGTCCACAGACTCCAGGACAACAGAGACATGCATGGCC
TGTTTGATGTGGATCTCTCTGACCGTCCAAGAGAAGCGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCAAATTCAGTGGAATAACAGGCGGAACCTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCCGGAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCTCAGACTGAATGAGAAACATTTGTATTTACATTAAATCCCCGT
TTTATCAGCGTCTTCCCGAGGACCCACCTACAAAAATAGGGGTCCTCTGGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCCGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCCC
ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGCCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG
GTGAAATGTAGGATGAATCACATCCCACATCTCTCTTTAGGGATATTAAGTCTCTCTCCA
GATCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGCCTGTCC
ACATGGGAGTCAAGTGTCTGCTGCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
TCAGGAATTCCTCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTPKIGVFLDYECGTISFFNINDQSLIYTLTC
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTSSESSQATTPLP
 REGM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGCCGCGGTGCGGAGGCTTCTTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCAGCCTGGCGGCCCTGCCTGTTGTGCTGCGCGCGCCGCCGCCGCCG
 CCGTCGCCCTCAGCCGCCCTCGGCCGGGAATGTCACCGGTGGCGGCCGGGCCCGCGGGCAGGTG
 GACGCGTGC GCCGGGCCCGGGTTCGCGGGCGAGCCAGCCACCCCTTCCTAGGGCGAGCGG
 TCCCACGGCCAGGCCCGAGGACCGGCCGCCCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTC
 ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGCGGAACGCACCTC
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCACTGGCCCG
 CGCCGACCACCCCTGTAGCGACACCGTACC GGCGCCACGACTCCCCGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCCTCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACGTGTAAACC
 TGCAAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGACCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACCTGAAGTTTATT
 TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAG
 GAGGATGAGGGTCATAGATTTACAAAAATTTTATATACTTTTATTCTCTTACTTTATATGT
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTTATGAAGAAT
 AAATCTGCTTCTCGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTCTTT
 ATGTTTATTAATATACCATTTGAGATTTGAGGAAATTTGTTGTTTATTTTCTCTCTA
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGCCAAAAG
 TAGATTAAGCAGGAATTTATCTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCATGAAAGTAATATTCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTGTGGACCCCAAGTCAAAAACCTGAAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTTGGGCAGTAATTTCTTTCACTGAGCTTGTTCCTTCTCAAG
 GTTGTGTGGAAGATTAATGATTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
 ACTTTGACTCCTTGACAAAGAAGTGCTTTTATACCTTAGCACTAAATTTTAAATGCTTTA
 TAAATGATATTATAGTGTATGGAATATTGTATCATATTTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGLLALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSP TTPPAERTS
TTSQAPTRPAP TTLSTTTGPAP TTPVATTVPAP TTPRTTPDLPSSSSNSV LPTPPATEAPS
SPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFY LNYTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCCTGGCTCCCGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

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FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAII FTQL
EFGDEFFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGACATGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACAGGAAGGCCTGTGTGTCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTACCTCGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTACCCCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAAGTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTCACCTGACAGACTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCCGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCTGTCCTTCTGCGTCACTCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAACGCTGTGAGGGGTTGAGCCT
 CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACCCGAGTACTCGGAGATCAAGATCC
 ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTAACTAAAAGACAGACAAATTCCTA

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FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVLTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTILIPQPDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVTFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDGTGIEDANAVRGSSASQGPLEPWAEDSPPDQPPASARSSVGEGLQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

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FIGURE 99

GACGCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

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FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTFLGVTLGAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSFVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

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FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
 GCGCAGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTACCTGCGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTGAGCACCA
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTAAAT
 AAGAAACCTAAGCCAAGACCTCTACGAACATTTCTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHNRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQLQGIISWGQDFCAITRKPGVYTKVCKYVDWIQETMKN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCGTGGAGCCGATGCCAAAAACCATGCATTTCTTATTTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACC GAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAGA
AGATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCATTTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGVQVIKGLDIAMTDMCPGKRRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNHDGDDGFISPKEYNVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT
 GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
 CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
 CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
 CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
 CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
 TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
 AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
 TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCCTCCCAAATAA
 AGTACTTATATTCTC

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FIGURE 106

MQGPILLPLGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCCTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGTACCTGGGAGCCTCGACGAGCCA
 CGAGCAGCACTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACCACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCTTTCAAGGTCTGGTGTCTTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
 CTGTTTCTCCACCTCCACCCCAACCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCTCCATCACTTCCCTAGCTCCACTCTTGTGGCCTGGGAACTTCTTGGAACCTT
 TAACTCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLI DHRWVLTAAH
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
 QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
 AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGCTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA
 GGACCCCGCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTTGTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACCAAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCCTG
 GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAAAATGCTACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAATAACAAGGTTGCTGTGCTGACCCCAATCTGCTTGAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEDLN
 NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
 MFEGKANESSPKFVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGACACCA**ATG**GCCCCCGGGTGGGCAAGGGTCGGCGCCGCCGTGCGCGCC
CGCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTTGAGTGGGCTCCAGCCGTGCGCTGCC
CACCAGATGTACTGCTGCTCCGCTGCCAGCTGGACTGCCAGGGGTGGCGCTCCGCGGGTTT
CTCGGGGATCCCCCGAACGCTGAGCGCCTTGACCTGGACAGAAATATATACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTGCATCTGGAAAGACAACAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCAGCGCGAAGCTCACCAGACTA
GATTTGAGTGAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATPCACCGATGT
GAAGAACCCTGCAACTGGACAACAACCATCATGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACGAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACTTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACTACT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCACGGCCCCCATCGGAGCGCCCATCTCGCAATGCCAACCATCATCTCCTGCCCTTCGCC
CTGCAGCTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTCGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAAGAACTCCATCAAAGCCATCCTTGCA
GGAGCCTTCAACCGATCAAGAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TCTTCCAGATGGCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGTGTCTCTCCTC
AATGCCAACAGATCAACGCTGCGGCTGCGGGTGAACGTTTCAGGAGCTGCAGAAGCAACTT
GCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCATTTGTGTGCGCATGCCACTTGAAGTGGGTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCTGCAGCAGCCCGCGCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAG
ATTACCGCAGAGGTTTACGACGCGAGTGCCTTCATGGACCTCGTGGCCCCAGAAGTGTCCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCCAGCCACCTCCC
TGAATATGTACCGACTCGCACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAAGT
GGAGACCGTGCACGGGCGGTGTTCCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTAGTAATGACACCTTTGCCGCGCTGAGTTCCGTGAGACTGCTG
TCCCTCTATGACAATCGGATACCAACCATCAACCTGGGGCCTTCAACACCGTTGTCTCCCT
GTCCACCATAAACCTCCTGTCAACACCCCTTCAACTGCACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCCCTAGGTGCCAGAAGCCATTTTCTCTC
AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCGCGCTGCCGAGCAGTGCACCTGTATGGAGACGTGGTGGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCGAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACTTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCACGCTTCAAC
GGGCTGCGGTCCCTGCGAGTGTCAACCTCCATGGCAATGACATTTCCAGCGTTCTGTGAAG
CTCCTTCAACGACCTCACATCTCTTTCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTCGAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTCAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGCAGTGGACATCAACATTTGTGGCCAAATGCAATGCCTGCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGTGGCTGGCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTACAGTGCTCTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCCAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTACGTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGTATGCGACGAGGTGATTGACCACCTGTGTGCCCTGAGCTGAACCTCTGTACGATG
 AGGCCAAGTGCAATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG
 AACACCCCCACCCATGGTCCCTACTGCAGACCCAGCCCATGCGACCCAGTACGAGTGCCAGAAC
 GGGGCCCAGTGCACTCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG
 CCTCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCAAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACTCCAAAGAGCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCTTGCGCCAGGGCACGG
 ACCGGCTCTAGCGGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCACCAAGTCCCTGGGGGTGTACACAGGCTGCAAGTCTGTACCCGT
 GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAC
 GCTGGACCGGCCACTCTGCGACAGGAGGCCGGGACCCCTGCCTCGGCCACAGATGCCAG
 CATGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGTTATGCATCATGTGCCACAGCCTCCAAGTGCCCATCATGGAATGTGCTGGGGGCT
 GTGGGCCCCAGTGCTGCCAGCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGGCTGCCTCGCGTGTTC
CTAAAGCCCCTGCCCGCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAGTATATTGTAAAAATAACAAAAAATAGAACTAAAAAAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRHSHNLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLRIDISKNIQSDIAPDAFQGLKSLTSLVLVYGNKITEIAK
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPFVCDCHLKWLDADYLDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLEPYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLSVCV
 SNDTFAGLSSVRLSLYDNRIITITPGAFTTLVSLSTINLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRLR
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLT LHGNDISSVPEGSFNDLTSLSHLAGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
 CEINPDDCEDND CENNATCV DGINNYVICPPNYTGELCDEVIDHCVP ELNLCQHEAKCIP L
 DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTCTC PQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS
 VELVTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIHEVRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

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FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAAGTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAAGTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA AAAAAGGCTGTGAGGTTTCT**TAA**ACTGGAAGTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAAGTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCAT
TTAAATGTC

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FIGURE 114

MKAAGILTIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCCTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAACTTGTACATGGCTCCC
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCTCTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**ATA**ATCAGATTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGGCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGATATTGCTCTTCTGTCTA
 TAAATTTGAATGATACGTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCAGATTCAAAT
 CCACCGAAGTGTCACTGTCTGTAGGGAATTTTGTGTTGTCCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGTGTTTATCATAAAAA

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FIGURE 116

MPLLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACGTGTGATGACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTAC
 TTGATAAAAAACATGACTCGGAAAAAACAAATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAACCACTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTCGAAGTCCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATATT
 CCTAGAGAGACCTCGTCCCTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGATATATGGTGACCACA
 GTACTTCTTAGTGATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 ATTAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

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FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
 ERYGPVVSFWFGRRLVSVSLGTVDLVKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK
 KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
 DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
 QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEVQKKLYEEINQVF
 GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETIVLYALGVVL
 QDPNTWPSPHKFDPDRFDELVMKTFSSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
 VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG
 TGGCCGCGCTCTCTGTCACCTTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA
 GTCTCCATGTTCAACAGACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCCGTCTTTGGGCTGAAA
 AAGAAACCCTTC**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
 ATTAATAAAAAAAAAA

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FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATGT**CCCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:
amino acids 1-20

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FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDFERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCYIAFYSTDYRLVQKVCPCDYNHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

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FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACCAGAGTGGGTGTCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG
 CATCTTCCCAGACACCGGGATCCCGGGGTAGGAGGCGACGCGGGCAGCACACGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
 GCGGTGCGGAGCACCAACCAGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCTTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGTAATTTGGTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAATCTAAAGTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAGAAGACTGTACTG
 TGTTAATATATTGATTATATTTGTTTTATTCTCTTGAATTAGTTGTTTGGTTCTTGTA
 AAAAATTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACTTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGCTTTTGTATAGTGCATATGAATTCATAAAATTTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

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FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFS AVRSTNHEPSEMSNKTRI IYFDQILVNVGNFFTTLESV FVAPRKG IYSFSF
HVIK VYQSQT IQVNLMLNGKPVISAFAGDKDVTREAA TNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGGCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCTTTGTGAATACCTTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDN
KDGPQTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNLTSLDGLPGTVGIHGDSPOFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCGCGGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATggtTCGCTCTGGGCTTGCCCTTCT
 TGGTGTCTTTGGTGGSCCTCGGTGCAGAGGCCATCTGGGGGTTCTGGGGGCCAAGAAGCTCTCCGAGAAAGACGCCG
 AGTTTGAAGCCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACCTGTGACCC
 GCACAGGACAGAGGGGCTGCGTGTGTCTGTGAACGCTCTGAACAGCAGAGAGGGGGCGCGTGTCTGTTTGTGG
 TCCGCGAAGAGGAGGTGTGGTGTCTTCCAGGTGCCCTAATCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAARAAAGTGAACGACACCTGTGTGACGCCCCCACCAGAAATGAGTCGGAGATTCAGTTTCTCTACGTGGATG
 GTCCACCTGTCAACAGTCAACACCATACAGCTCCGGCTCAGCCGATGGACGATTTGTGTCTCAGGACTG
 GGGAGCAGTTTCACTTCAATACCACAGCAGCAGCCAGTACTTCAAGTATGAGTTCCTGGAAGCGGTGGACT
 CGGTAAATTGTCAAGGTGACCTCCAAACAGGCCCTTCCCTGTCTCAGTCACTTCCATTCAAGGATGTGTGTCTGT
 TCTATGACCTGGACAACAACGTAGCCTTCTCATCGGATGTACCAGACGATGACCAAGAAGGGCGGCATCACCCTAC
 AGCGCAAGAGACTTCCCGACCAACAGCTTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTCGGGGGCT
 CCGTGCCCTTCTACCCCTTTCGACAAGATGAACCGTTCGATCAAGGGCACCAGCAAAACCTGTCAAGTGTGG
 TGTCTCAAGCAGTCACTGTGAGGCATACGTCACTGGGATGCTCTTTGCTGGGTATATTCTCTCCTTTTACC
 TGCTGACCGTCTCTGCTGCTGCTGGGAGAACTGGAGGCAGAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
 CTTGCCCAAGAAGCGGTCAACCCTCGAGTCTGGCTGATTCTTTCTGGCAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGGACCTCTCTTACG
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACCTCATGAGCTCTGTGGAGGAGGAT
 ACTACGACGATTTGACCGCATCGATTCCGACAAGAATGTCTTTCGACCAAGCAATACCTCTATGTGGCTGACC
 TGCGACGGGAAGGACAGCGGTGTTTCTGCGGAAAAAGTACAGATCTACTTGTGAAGAAATGGCCAACTTGTCT
 TCTATGCTCCTTCTGTGGTGCAGCTGGTGATCACTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
 GCTACTACAACTTCTCTGCGCCACCACTGGGCAATCTCAGCGCTTCAACCAATCTCTCAGCAACTCTGGGT
 ACATCTGCTGGGGCTGCTTTTCTGCTCATCTCTGCAACGGGAGATCAACCCAGCCAGGGCCCTGCTGCGGCA
 ATGACCTCTGTGGCCTGGAATGTGGGATCCCCAAACATTTGGGCTTTTACGCCATGGGCACAGCCCTGATGA
 TGGAGGGGCTGCTCAGTGCTTGTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGAACATCGTTCAATGT
 ACATGATCGCGGACTCTGCATGCTGAAGCTTACAGAAAGCGGCACCCGACATCAAGCCAGCGCTCAGATG
 CCTACGCTGCTGCTGGCCATTGTCTCTTCTCTGTGCTGGGCGTGGTCTTGGCAAAGGGAACACGGCGTCT
 GGATCGTCTTCCATCATTTACATCATCGCCACCCGTGCTCCTCAGCACCGGCACTATTACATGGGCGGTGGGA
 AACTGGACTCGGGGATCTTCCGCCGATCTCCACGCTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCGGC
 TCTACGTGGACCGCATGGTGTCTGGTTCATGGGCAACGTCACTCAACTGGTCTGGCTGCCATCGCCCTTATCA
 TGCGCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCTTACTTCGCTTCTCTACA
 TCTATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCGCTGCTCTGCATCGTTTGCACTCCGTGGTCT
 GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAAACCCCTGCAAGATCGAGGGAGACA
 ACCGGGACTGCATCCTCTCGACTTCTTGACGACCAAGACATCTGGCACTTCTCTCCTCATCGCCATGTTTCG
 GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGACGCGGACAAGATCTATGTCTTCTAGC
 AGGAGCTGGGCGCTTGCCTTCACTCAAGGGGCGCTGAGCTCCTTGTGTGCTGAGTGGCTCACTCTGTCTGTGCT
 GTGGGAGTGATGCCAGCCGCTGCCAGCACTGGATGGCAGCAGGACAGCAGGCTAGCTTAGGCTTGGCTCT
 GGGACAGCATGGGGTGGCATGGAACCTTGCAGCTGCCCTTCCGAGGAGCAGGCTGCTCCCTGGAACCCCC
 AGATGTTGGCCAAATGCTGCTTCTTCTCAGTGTGGGGCTTCCATGGGCGCTTGTCTTGGCTCTCCATTT
 TGCTCTTTTCAAGAGGAAGGATGGAAGGGACACCTCCCAATTCATGCTTGCATTTTGGCCGCTCCTCTCCCC
 ACAATGCCCAAGCTGGGACCTAAGGCGCTCTTTTCTCCCAATCTCCCACTCAGGGCGCTAGTCTTGGGCGCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTGGGCTGCTCTGGCTGCGCATCTGCAATTCAGTCACTGAGC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGTGAAGCGCTGCAAGGGG
 CTTGGGGCAGTGCATTTCTTCTCCTCTGACCTGTGCTCAGGGCTGGCTTTTGAACATGGCTGACCCAAAT
 TGAAACCGCTCTGATTTCAAGAGGCTGAATTCAGAGGTCACTTCTTATCCCATCAGCTCCGACGATGCC
 AGCACAGGACTGGAGGAGAGCGCCTCACCCCTTCCCTTCTTCCAGGGCTTAGTCTTGCCAAACCTCC
 AGCTGGTGGCCTTTCAGTGGCATTGACACTGCCAAGAATGTCCAGGGGCAAGAGGAGGATGATACAGATCTCAG
 CGCGTGTGCTCCACAGCTGTGGGCAACCCAGTGCCTACCTTAGAAGAGGGCTTCAGGAAGGATGTCTGTTT
 CCGCTCTACGTGGCCAGTCTAGCTCGCTTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGCTCTCAGGCA
 AGTCTGTGTAGTCATGCACACATACCTATGAACCTTGAAGTTTCAAGAATTCGCCAGCTCTGGCGAC
 CTTGGCCACCTCTGCTTCTGGATCCCTCTGTCGCCACCTGTGTCAACCCAGATGTGAGGATGGGGGAGCTCAGG
 CGGGCGCTTGTGTGGGATGGGAATGTTTTCTCCAACTGTGTTTATAGCTTCTGCTTGAAGGCTGGG
 AGATGAGTGGGTCTGGATCTTTTCTCAGAGCTCTCCATGCTATGTTGCAATTCGCTTTTCTATGAATGAAT
 TGCATTCAATAAACACCGACTCAAAAAAAAAAAAAA

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FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGLVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVNLNKQKGAPLLFVVVRKEAVVSFQVPLILRGMFQRKLYLQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFEGVDSVI
VKVTSNKAFCPSVISIQDVLCPVYDLNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYFFAEDEPVDQGHRQKTLISVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPEGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLISYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQT VVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPTNFQFDTSMFYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFIIHIIATLLSTQLYYMGRWKLDGIFRRLHVLYTDCIRQCSG
PLYVDRMVLVVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTDDDDLDTVQRDKIYVF

```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTGCTTGGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCTTGCTCTG
 ACCATGGTGGCTGCTTGGCTGGCTGTGGCTGCTTTGTGCTCCGTCGCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACATAGTTGGAAATTTCCCTTTATACC
 TGACCAAGTTGGCCCTGCCCGCTGAGGGGGCTGAAGGCCAGATCGTCTGTCAAGGGGACTCA
 GGCAAGGCCAATGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCGTGCTGGTGACCA
 GGCCCTGGACCCAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCTTGGAGATGCAGGATG
 GACATGCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGGCTGGCATCCC
 CTTCTCTTCTTGGGCTTACAGACCGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCTTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGGTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTTATACCCGACCCACATGGCCAGGTACACTGGAGTGGGGGTGATGT
 GCACATACCTTGAGAGGCCATCCCCCGGAGCCCTTTGAAGTGAATGCAGAGGGGAAACCTT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACACGTGCGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTGATGAAGTGAAGTGTCTGACAGCAGGATGACAGTGCCTCCGCGCTCCCCCAATTCC
 CACGTGTGTATGACTCTGAGCCCTGAGCCTGAGGATGGGGTGAAGGGGAGACCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGTGTCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGGTGTGCGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGCTGT
 GAAGTCGAAGTCGCAGTCAAGATATCAATGATCACGCCCTGAGTTTCATCTTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGAGCTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCTCATGGATTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCAAGGTTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGGCCCC
 AGCGGCTCTTTCTGCTGACCATCCAGCCTCCGACCCATGACCCGAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC
 GCCAGTCCCTGCAAGGCGGCCAGCCTGGGGACACCTACACGGTGTCTGTGGAGGGCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCCCTCCCAATACCTTGACACACCCGCCAAGACCATG
 GCTTGATCGTGAAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGACCGGTCCTTACAG
 TTCACCTTGGTCCCAAGCCACGGTGCACCGGATTGGCGCTCCAGACTCTCAATGGTTT
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCGAGTGATCGTGTGTGCTGCAAC
 GTGGAGGGGCAAGTGTGCGCAAGGTGGGCGCATGAAGGCGATGCCACGAAGCTGTCCGG
 AGTGGGCATCCTTTGATGGCACCTGGTAGCAATAGGAATCTTCTCATCTCATTTTACCC
 ACTGGACCATGTCAAGGAAGAGACCCGATCAACAGCAGACAGGTCGCCCTGAAGGCG
 ACTGTCTGAATGGCCCGAGCTAGCTGGGAGCTTGGCCTTGCATCTGAGTCCC
 CTGGGAGAGAGCCAGCACCAAGATCCAGCAGGGGACAGGACAGAGTGAAGCCCCCTCAT
 CTGCCCCGGGGTGGAGGCACCATCACCATCACAGGCATGCTCTGCAGAGCCTGGACACCAAC
 TTTATGAGCTGCCCATGGGAGTGTCTCAAATGTCAAGGTGTTTGGCCAATAATAAGCCCCA
 GAGAAGTGGGCTGGGCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 132

MVPAWLWLLCVSPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRPDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAQVDPTSGSVTLGVLPLRAGQNIILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEV VVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLLTIQPSDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQMWQLLVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATCAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCT
 TCAATCGGCCTGTGGATGTCTGGTCCCATCTGTCACTGTCAGGCAATTTAAATCCTTCTCT
 AGATCCCAGGGCTTAGAGTACGCACTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTCACTACGGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGTTGAAGATTGGACATTCGTTTGAARACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGCGTGAGGGCGGCCGCCGTTTGGCTGAATGCAGGCATCCATTTCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAATGGATATTTTCTTGTGCGCTGTGGCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTTTGCAAGAAAG
 GGAGCCAGCGACAACCTTTGCTCCGAAGTGATCCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGGCTTCATCGACCTGC
 ACAGCTACTCGACGTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCGACATGCG
 GAGGAACTCGACAAGGTGGCGAGGCTTGGCGCCAAGCTCTGGCTTCTGTGTGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGG
 TTCCTCCTGCCAGCTAACCGAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATCAACCCCTTCTGGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTTCCATCCTGTGTGAG
 TCAGAGCCCTCTGGGTTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCTGGCGGTGTCCTTGCAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGCGGCTGCACTC
 AGCATCAACCCCTTCTGGGTGGCATGTCTCTACCTCATTTTGAAGCAAGAACATC
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCTTAATTTT
 TCGCAGTCTTCTGGAAAAATTTTCTTTTGGAGCAGCAAATCTTGAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCTCTTTTTTTTTTTTTTGTAGACAGAGTTTGTCTTGTGTGCC
 CAGGCTGGAGTGTATGCTGCATCTGGCTCACCACAACCTCTGCCCTCGGGTCTCAAGCA
 ATTCCTCTGCCTCAGCCTCTTGAGTAGCTTGGTTTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTTGTGTTTTTGTAGTAGAGCAGGGTTTCTCCATGTTGGTCAAGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCTTGGCCCTCCAGAGTGCTGGGATTACAGGTTTGTAGGCCACTG
 TGCCGGGCGGCTCCCTCTTTTTTTAGGCCGAATACAAAGTAGAAGATCACTTCTCTTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCTAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTCAGGATGGTGAAATTTATCCCCATCTGTCTTAATGGGCTTACCTCCT
 CTTTGGCTTTTGAATCACTTCAAAGATCTAGGCCCTCATCTTACAGGTCTCAATCACTCAT
 CTGGCGTGATAATCTCACTGCCCTGGCACATTCCTATTTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTCGTTTTGT
 TCTGTCTATTTTGTATCTGGACCAAGTTTCTAAGTAGAGCAAGAATTCATCAACCAGCT
 GCCTCTTGTGTTTCACTTCACTCAGCAGTACCATCTGTCTCTTTTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTTAATCTTAACCTCTGCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

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FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPLARRVKIGHSFENRPMYVLKFSTGKGVRPPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRRWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

[illegible]

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FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEA EVFSTDFSNP SIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFI PRF
SISASYNLETILPKMGIQNAFDKNADFSGI AKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

[illegible]

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FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTNNGVSIVTNNEFHTTSSGISTATNNEFSTASSGISIATNESSTTSSGASTATNSE
SSTPSSGASTVTNNGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSS
TTSSGASTATNESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNESSTT
SNGAGTATNESSTTSSGASTATNSDSTVSSGASTATNESSTTSSGASTATNESSTTSS
GASTATNSDSTTSSGAGTATNESSTVSSGISTVTNESSTPSSGANTATNESSTTSSGA
NTATNESSTVSSGASTATNESSTTSSGVSTATNESSTTSSGASTATNSDSTTSSEAST
ATNESSTVSSGISTVTNESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAGLFFAGLFFCVRNSLSLRNTFNTAVYHHPGLNHGLGP
GPGGNHGAHRPRWSPNWFRRRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAGCGGTCCAAGGGTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTGGGGGTGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTTGTGAATAAACTTGATACACCA

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FIGURE 140

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

CCCGGGGTCCTCCAGGGGGCTCCGCCGGGGCCGGCCCTGGCCGGGGGACGAGTCACTGGACACTCTGGGAAGAGCGGCC
CCCGGGGGGGGAGTCAAGCTCGCTGACCTTCACTTCACTCAAGCTCCGAGGCGGGGCCCCGGGCSACTGCG
GGGGCCGAGCCGCGGGGCGAGCTCGCCGCCGTGAGTCCGGCCGAGGCCACTGAGCCGAGCGCGGGAGACCCGTCT
GCTCTGCTCTTCCGAAGCTGCGCACCGGACTGGGCTCTGAGGAGCTGGCTCGGCCGCCCTATGGGGCGGCTGCGCG
CTCTGGCCACCCGCTGCTCTGCTCTCTGCTGCTGCTCTGCTGACCGGCCGCTCGACCTGGGCGCTCAGC
CCCCGATCAGCTCGCTCTGGGCTCTGAAGAGCGGCATCTCTCAGATTGGAAGCTGAACACTCTTCAACTAC
ACAGCCCTTCTGCTGAGAGGAGTGCGAGGACCTCTAGCTGGGTGCTCGAGAGGGCCCTTTTGCATCTACGAG
AACCTCAGGCTTCTCGGACGGGGGATACAGGAGGCTGCTTTGGGTGCGAGACGAGGAAGAAGAACAGAGTGC
AGCTTCAGGCGAAGGACCAAGCCGAGCTGTGTAACATACATAAGATCTCTCTCGCGTCAGCGGAGCTAC
CTTGTCACTCTGGGCACACGAGCTCTCAGCCGCTCTGCTACTACATTAACATGAGAACTTCAGCTCGGAAG
GACGAGGAAGGGGAATCTCTCTGGAAGATGGCAAGGGCGTCTGCTTCTCGACCGAATTCAGTCACTCTGCC
CTGTGGTGTGATGGGAGCTCTACATCTGAAGACATACGAGCTCTCAAGGAATGACCCGGCATCTCGCGAGCT
CAAGGCTTCTGCCCCCAAGAGCGAGCTCCCTCACTGGTTCGAAGACCCAGCTTTTGTGGCTCAGGCTAC
ATTCTTGAGAGCGTGGGCGAGTTCGAAGGCGATTGATGACAGATCTACTTTTCTCAGGAGCACTGCCCAGGAA
TTTGAAGTTCTTGAGAACACATTTGTTCGCCGATTCGCCGATCTGCAAGGGCGATGAGGTTGGAAGCGGGTGT
CTACAGAGCGCTGGACCTCTCTCTCAAGGCCAGCTGTGCTGCTCAGCGCCGACGATGGCTTCCCTTCAAC
GTGCTCGAGGATGTCTCAGCTGAGCCCGACCCCGAGGATGGGCTGACACTTTCTATGGGTTCTTCACT
TCCGAGTGGGACAGGGGAATGACAGAGGCTCTGCCGCTGTGCTCTTCAATAGAAAGTGTGAGAGAGCTCTT
AGCGGCTCTACAAGAGGTGAACCTGTGAGACACGAGCTGGTACACGTAACCCCGTGCCACACCCGGG
CTCGAGGCTGCATCACCAAGATCGCCGGGAAGGAAGATCAACTCTCTCTCGAGCTCCGACAGCGGCTGTCT
AACTTCTCAAGAGCACTCTCTGATGGACGGGAGCTCGGAAGCCGATGCTGCTGCTGACGCCACCGCTGCT
TACCGCGCTGGCTCTACACCGCTCTCCCTGGCTCGACACACATAGATGTCTCTTCTCTGGGCACTGTGAC
GGCCGCTTCCACAAGGCACTGAGCTGGGCCGCTGGGCTGGCTGACATCTTGAAGAGTCGATCTTCTCATCGGA
CAGCCGCTTGCAAAATCTCTCTGGACACACAGGGGGTGTCTGTATCGGCGCTACACTCGGGGCTGATCGAC
GTGCCATTCGGGCAACTGAGCTGTATCCGAGCTGTGGGAGTGGCTCTCGCCGGCGAGCCCTACTGTGCTGG
GCGGCTCCAGCTGACAGACGTGAGCTTACCGGCTCAGCTGGCCACAGGCGCTGGATCCAGGAGATCGAG
GAGGACGCGCCGAAGCACTTTCAGCGGCTGTCTGGTTGTCTCCGCTCTTTTGTAACCAAGCGGAGAAGCCA
TGTGAGCAAGTCAGATTACAGCCCAACACAGTGAACACTTGGCCTTGGCCGCTCTCTTCAACTCTGGGCAACCG
CTCTGGTACGACAAAGGGGCGGCTCAATGGCTCGGCTCTGCAAGCTGCTACCACTGGGCACTGTGCTGTG
GTGGGCAACCAACAGCTGGGGGATTCGATGCTGTGATCAGAGAGAGGGTCTCCAGAGCTGATTAGGCCACTAC
TGCCAGAGGTGTGTGAGGACGGGGTGGCAGACACCAAGATGAGGTTGGGCAAGTACCCGCTCATATCAGCACA
TCGGTGTGATGTACCAAGCTGTGGCAAGGCCAGTGGGTTGCAAGAGGCTCTACTGGAAGGAGTTCTGTGTGT
ATGTGACGCTCTTTGTCTGGCGGTGTGGTCCGATTTTATTTCTGTCTACCGGCAAGGACAGCATGAA
GCTCTTCTTGAGGACAGGGGAATGTGCGAGCTGTGACCCGAAGACTTGCCTTGGTGTGCTCCCTGTAGAGCCGC
GCATCTAACGGCTTAGGGGCCCTTAGACCCGCTGATACCGAGGTTACGATCCGTGTGACAGACGCCCGCC
GGGGCCGGAGTCTTCACTGAGTCAGAGAACAGGCCACTCAGATCAAGAACAGCTTGTGGAGGATATCCCGAT
TGCCCCCGGCGCGGTGCGCCTTGGCTGGGAGTCTGCTGACTGTGTGGTGTGAGAGACTTCCAGGAGGAC
TGCCCTGCTCTCAGGGGCTGTAATGCTCGGAGAGGTTCAACTGGAATCTCCCTTCGCTCTGCTCTTCTGTGG
ACGACGCTGTGTGGCGGCTCTGGGAGCTTGGAGAGCTTGGCCTGTGCTGTCTACGTACAGTACGGAAGCTTC
TACCCACGACAGACCAACAGCCGCTGGCCCGAGAGTCTCGCCCAAAATATGGGGCGGCTGCTAGGTTGTGTGAA
CAGTGCCTCTTATGTAAATCAGGCTTTGTTTAAAAAACATCAAATGTGAACTAGATGAGGAGGAGAT
ATAGATCACTGACGACACACAGGCTGTCTCAGTTCTAGGCTTCCGAGGGGTCTGGGAGTGCATCAAAGTGG
TTGTTGAGACAGATTTGGAACCTTCAACATGGCTCTTCACTTCCAACTATCCCGTGCACCCGGCTGCT
CTGTGTCTCACTGAGATCAGGACAGGCTTGGGCTGGCTGCTGCTTGCCTTCAAGCTCAGCCGAGGATGTAGTTG
TTGTTGGCTGTGCTCCCACTCAGGACACAGGCACTAGGTTGGCATCGCGGCTCAGAGCTCTGGGCT
GGACCCACTCTTGAGCTTTCCAGCTGTATGACGCTGTGGCCACAGGAGACGCGGAGCTCAGGAGATA
TTTCTGACAATCTGAGCCTTTCTCCAGAATTCAGGAAGAGCTCTGCGCTGCTTCTCGCTGTGTGCTGTG
GAACCCGCTTGGCCCTTCCCACTATCCACTCTGCTTCACTTTGAATCAACACAGGAAGTAATGCACTGC
CTGGTCTTCTCCCGATCCCGATTCACCTCCATCCCTCACTTCCCTCACTTCAAGGATATCAACATGCC
AGCAACGGGGCCGTAATTTATGTGTTTATTATATTTTATATAGATGCATTTATGTCTATTTTATATAA
GCTCGAAGATTAAGCTTTTAAAAAATAAAAAA

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FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLEEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSLRPKTESLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVR
SRMLLLQPQARYQRVAVHRVPLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR
PLSIQDSFVEVSPVCPFRVRVLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGCGGCGCCGGCTACGAAGAGGACGGGGACAGGCGCGGTGCGAACCGA
 GCCCAGCCAGCCGGAGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCCGCTCGTCCGCGTCTG
 TGGCCGCCCGCGTCCCCCGCGGAGCGGGAGGAGCCGCCACCTCGCGCCCGAGCGCGCCGCTAGCGCGCGCG
 CGGGCATGGTCCCCCTCTTAAAGGCGCAGCGCGCGGCGGGCGGGCGGGTGTGCGGAACAAAGCGCGCGCGGGG
 CTTGCGGGCGCTCGGGGCGCGCATGGCGCGCGGGCCCGCGCGCGCGCGCGCTGCCCGGGCGGGCTCTG
 CGCGCTTAGGGCGGGCTGCGCTCTCGTGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCTGCGGGCGGGCGG
 GCGCGCGCGCGCGCGCGCGCGGAGCGCGCGCGGCGCTGGCGCGCTGGCTCAGCGTGC
 TGCTCGGGCTCGTCTGGGCTCTGCTGTGGCTCGCGGCTCGTCTCGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCACGCGCGCGCGCAGCCAGCCGAGGGCTGCGGTCGGGCGAGCGCGCGCTTCCAGGCGCGCGGGGCGCGG
 GCGATGCGCGCGGGGCGCAGCTCTGGCGCGCGGCTCGGACCCAGATGGCGGCGCGCGCAGGAACTTCTCT
 TCGTGGGAGTCATGACCCGAGAAATACCTGCAGACTCGGGCGTGGCGCGTACAGAACATGGTCCAAGACAA
 TTCTGGGAAAGTTTCACTTCTTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGACGACTCCTACCCGCCCGAGAAGAAGTCTTTCATGATCTCAAGTACATGCACGCCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGAGGAGCCGCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCTCTTCTTGGCGAGCAGGCTGGGACCCACGGAAGAAATGGGAAACTGGCCCTGG
 AGGCTGGTGAGAACTTCTGATGGGGGGGCTGGCGTGTATGAGCGGGAGGTGCTTCGGAGAAATGGTGCCG
 CAGGGGTGCGATGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTATGAGAAATACGAGCAGAAACGGGGT
 ACATTAGAGATCTCCATAACAGCTAAATTCACCAAGCTATCACATTACACCCCAAGAACCAACCTACCAAT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGACAAATACAGCTGCACCGGAA
 TTGCTCTGATGAGCAAAATACGCAACACAGAAATTCATAAGAGGAGCTCCAGCTGGGAATCCCTCCCTCTTCA
 TGAGGTTTCAAGCCCGCGAGCGAGGAGAGATTCTGGAATGGGAGTTTCTGACTGGAAATATCTGTATTGCGGAG
 TTGACGCGCAGCCCTCGAAGAGGAATGGACTTCGCGCCAGGGAAGCTTGGACGACATTTGCTATGACGTCA
 TGGAGATGATCAATGCCAACGCCAAGACAGAGGGCGCATCATTGACTTCAAAGAGATCAGTAGCGGCTACCGCG
 GGGTGAAACCCATGTATGGGGCTGAGTACATCTTGACCTGCTGCTGTGACAAAGACACAAAGGAAGAAAA
 TGACGGTCCCTGTGAGGAGCGACGCTATTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGGCCAAAGGAATCAATCAGGAATCTGGATCTTGTCTTCTCAAACTCCCTGAAGA
 AGCTCGTCCCTTTCACTCTCCCTGGGTGGAAGAGTGAGCACAAAGAACCAAAGTAAAAAGATAAATCAATGA
 TTCTTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAAT
 AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTTGACAAGCGCAAAAGTTGAAGTGATGA
 GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCGAGATTTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCGTGAAGTAGGATCTCCAGTTTAAACAAATGAATCTTGTCTCTTCTTGGCAGCTGCACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGATGTGAGGAAATACAGTTCTGGGCGCAACAAATATATTTTCAATCATCTTCAAGCAGT
 ATGACCCAAAGATTGTTTATGAGGGAAGTTCCAGTGACAAACATTTTGGCTTTACTCAGAAAGAACTGGCTTCT
 GGAGAAATCTGAGTTTGGCATCGGTGATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAAGTTGTCCAGGACAGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGCTCCACATCTCTGCTTTTGTGATCCCAATTTGACCCCAACAGTACAAATGT
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA
 TTACAGATTCATTTTATTTTCAAAATTTTGTGATGATCAGTTTGAAGTCCGATGATCAAGGATATATTTTAC
 AAGTGGTTTCTTACATAGGACCTCTTAAAGATTGAGCTTCTGAACAAGAGGTGATCAGTGTGGCTTTGAC
 CACATCTTCTTGTGAACATTTATGTTAGCAGACCTGCTTAACTTTGACTGAAATGACTGATGAACAAACATTT
 TTTTAAAAAATGTTTCTTTTGAAGCTTTGCTCCAGTCTTGGCGAGAAACGTGAACATCTTCAAGAAATGT
 TATTTGTGAACAAACACGTGAACCTGTTGAATGTTCTGTGTGATGTAAACATCCACAGATTTACCTTTTGT
 GTTTGTGTTTTTTTTTTTAAATCTGTTTAAAGCCATTTTCTGTTCCAGTTTGAAGATAGGAATGTGATAATA
 GCTGTTTCATCATTTGCTTCAGGAGAGCTTCCAGAGTTGATCATTTCCCTCTCATGTTACTCTGCTCAGATGGC
 CAGTAGGTTTTTTTGTGTTTTTTTTTTTTGTTCTTTTTTGGAGCGGAGCTCACICTCTTACCCAGCGTGAAT
 CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTCAAGCAATTCCTCGCTTTGGCTCCCGAGT
 AGCTGGGATACAGGCACACACCACCGCCAGNTAGTTTGTATTTTAGTAGAGCGGGTTTCCACAT
 GCAGGCGCAGCTGGCCAGTAGGTTTAAAGCAGGGGCGTGAAGAAGGCACAGTAGGATGTGGCTCTCTCTG
 TGGTAGTTCAATCGGCTCAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTTCTCTCTGACCTT
 CTCTTTAAAGGGTAAATATTAATGTTTAGAATGACAAAGATGAATTTTACAAATAAATCTGATGTACAGAGAT
 GAACATACACACATACACCTTAATCAAAAGTTGGGGAAGAAATGTATTTGTTTGTCTCTTATCCTGCTG
 TGTATGTGGGTGGAGATGGTTTCTATCTTTCATTACTGTTGTTTATCTGTGATCTGAATACCTTTAA
 TTTATTTAAGTCTGTGTTGTCAGAGCTCTGCCATTTCTGAGTACCTGTGATGTAGTATGTTATGCTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCAAGAAATTTCTTTGGAAACGCTTTTCCCCCTC

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FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPFGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGKYLKYSYAVDGGPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHPVFCDPNLDPKQYKMC LGSKASTYGSTQQLAEMWLEKN DPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

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FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTG
 ACCGCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATGG**CCTTTTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCTCTTTCTCGAGACCAAGTGCAGAGGCTATGGAAGTGCGGTCTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGGAACTGAGTTTGTGAAGGACTCCATTGCAAGGGGGCGTGTCTCTTAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCTAGTCCCGAGTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCTATTTCCTAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCCGAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTCTTCAAATCCAAAGGGAAAAATCCA
 GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGGAATTGAGAGACGCCCGGAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
 ACTTTGCTTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAATTTGATATTTTAC
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAGTTTGAAGGCTTGTGAGACCTATATCCAGCATCCGATAGTAGACGA
 GGAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGCGGAT**AG**ACAGAGAAAGCCCTG
 CTTAAAGGGCCCCACACACAGACCCAGACAGAGTCAAGGAGAGATGCTCCCGACAGGTGGC
 CCCAGCTTCTCTCGGAGCCTGCGCACAGAGAGTCAAGCCCCCATCTCCTTATGGGAGC
 TGAGGTTCTTCTGCCCCTGAGCCCTGCAGCAGCGGCAGTCAAGCTTCCAGATGAGGGGGGAT
 TGGCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAAACAAGTCAACCTCC
 CAGGCTCCTCATTTGCTAGTCCAGGACAGTGATTCTGCTCAGAGTGAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTGTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTATTCCACATTAATTTACTTTTCTCTA
 TACCAAAATCAACCATGGAATAGTTATGAAACACCTGCTTTGTAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTCTACTGATTCTATAAGCCAGCATTACCTGATACCAAAACAGGCAAG
 AAAACAGAAGAAGAGGAAAGGAAAACTACAGGTCCATATCCCTCATTAAACAGACACAAAA
 TTCTAAATAAAAATTTAAACAAATTAACATAAACAAATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTTGTCCCACAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAAGTGTAAAT
 CAGCACATTAATAAGTAAAAAAGAAACCATAAAAAAAAAAAAAA

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FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTTGTTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA
 TTACTATAGCACATTGTCATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTTATAAA
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAAATAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCCATCATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGA CTCTGGAGGACCCTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAAACAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCTGCTTCTG
 CCAGATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGCAGAATTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTAGCAAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCAATATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACATAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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FIGURE 150

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop .
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTD
KLYAEFGREASNNFTMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNLHRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

GTCTGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTTGGGGATCCCTCAGCCTAACACCCACAGACGTGACGTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGCTCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCCTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCAGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGCAGCCGCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGAGGGGGCGCTCTGA
AAGGGGCTTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAGAAGGAAAAACCGCTGCCCTCAGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCAGAGGCCACGGCGGAGTCATGTTCTCTCAGGACTAGAGCCTGTTTAGTCCGGTACTT
GGCGCTTTGTTTCTCGCTGAGTGTCTGGGAAGGAATAGAAGGGGGCCCCCAATTTTTTTTA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGSSPAQPPDPFRMGVEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPLNATVRRRELKGLKPGGIYVVCVVAANEAGASRVPAAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDWRGCPRRAAAAAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGG
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACAAATGGGCCAGAGAAGATTCCCGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTTCTGCTTGGAA
 TGGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCCCTGTGGTTCATCCGGTCATGATTGCTGTTTGGCTGTTTCCCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCACTTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
 CTTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCAATGTCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGAAAAAGTTTCATGTCTAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGTATAGCATTTTC
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATGTAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTTCTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTAA
 TCTGTATAAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATATGAAAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTTAGCCTTTCTGTAAATAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
 CCAGTGTGATACATAGGAATCATATTACAGAAATGTAGCTGGCTTTAGGAAGTATTAATAA
 GAAATTTGCACATAAATAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCAAATG
 AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTCCTTCTCCAAACAGAA
 GCAATAGTCTCCAAGTCAATATAAATTTCTACAGAAATAGTGTCTTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTTAGAGATCTTTGTTTTTTTCACTGATTA
 ATATACTGTGGCAAATTCACAGATTATTAATTTTTTACAGAGATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTCTCAGAAATATGGAA
 AGAAAATTAAAAATGTGTCAATAAATATTTTCTAGAGAGTAA

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FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSPLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
ACCGGGAGGATCACAGAGCCAGC**CATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
CCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
TGATTCTGGATAAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
ACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
TGTTGTTGAAATCAGAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCCTGAAGACCCCCCGT
GTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGCCCTTGGCAGGTCAGCATCCAGTACGA
CAAACAGCAGCTGTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACT
GCTTCAGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
AGCTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCACCCCATGTACCCCAA
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGC
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGA
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCCTCAGTCCA
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
CTGATGTACCAATCTGACCAGTGGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
GGGCCCCAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTCTG
CCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
CTCTGCCCACAGCCTCAGCATTTCTTGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCC
TCGACGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCCACTTGGTGTCTCC
AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAAGGCCAGATCACTGTGGG
CTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
CTGGCAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYFF
 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
 SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNRSSGPCLSGSLVSL
 HCLACGKSLKTPRVVGGEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
 FNWKVRAGSDKLGSPSLAVAKIIIEFNPMYPKDNIDIALMKLQFFLTFSGTVRPICLPFFD
 EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAQQGEVTEKMMCAGIPE
 GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGAAAGCCTGGCATTCCAGAGGAGGGAACGACGCGGCATCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCGCTGGACCCCTGGAGCCTCCTGGGCC
 TTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGGAGGGGCCATGCCA
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAAGAGGGCCTCCAGGATTTTGACA
 CTCTGCTCTGAGTGGTGATGACCAATAGCTCTACGTGGGGGCTCGAAGAGCCATCTCGGCTTGGATATCCAGG
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCGTGTCTGGTTCTTACAATGTCAACCATCTCTACA
 CCTCGGGCACCTTCGCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTCTGGAGGAAAGGCCAAAGCCCTTTGACCCGCTCGACAGCATACGGCTGCTCTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCGAGC
 CTGTCTCAAGACCGACAACCTCCTCCGTGGCTGCATCATGACGCCTCCTTTGCGGAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTCGAGGAGACGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAATGACGTGGCGGCGAAAGCTGCTGCAGAAGAAGTGGACACCTTCTGAAGGCCGAGC
 TGCTCTGCACCCAGCGGGGAGCTGCCCTTCAACGTCTATCCGCCACGCGGTCTGCTCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTACGCACTCTTCACTCCCACTGGCAGGTGGCGGGACAGGAGCTCTGCGGTTGTGCTCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAGAGTTGAACAAGAAATCTACGCTGGACTA
 CTTATAGGGGCGCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGCCCTCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGACGCCCCCTGCTGGTGAAATCTGGCGTGAGTACA
 CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTAACCTGGGAACCAACACAG
 GGTGCTCCCAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTCAGAACTGACGTGGCGGCCCAACCCAGGGTGCAGTGTTTGTAGGCTCTCAGGAGGTGTCTGGA
 GGGTGCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCACTGTCCT
 GGGACCTGAGTCCGAACCTGTGCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCTCAGAGCCGCCGCAATCATTAA
 AAGAAGTCTGGCTGTGCCAACTCCATCCTGGAGCTCCCTGCGCCCACTGTACGCTTGGCCTCTTATTATT
 GGAGTCATGGCCGAGCAGTCCCAGAAGCCTCTTCACTGTCTACAATGGCTCCCTCTTGGCTGTGTCAGG
 ATGGAGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACAGACCCCTGGCCCTGGATCCTGAACCTGGCAGGATCCCCCGGGAGCATTGTGAAGGTCCCGTTGA
 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTCTACTGGCCCACTTTGTCACTGTCACTCTCTCT
 TTGCCTTAGTGCTTTAGGAGCCCTCATCATCCTCGTGGCTCCCCATGAGAGCTCCGGCTCGGGGCAAGG
 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAGGACCTTGCCAGTGATGTGGACGCTGACAACAACCTGCCTAGGCATGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGCTGCGCTGAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAGACCACTTTCTTCCCTGAGAGGAGCTTCTGCTACTCTGAGGAGCTCTGATGACCTCAGGAGGAGTG
 ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCAGGGGACCTC
 CAGAAACACAGTGTTCAAGAGACCCTAAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAAAACAT
 TAAACAATCATATGCTTAACATGCCACTCCTGGAACTCCACTTGAAGCTGCGGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCATGCAGGGATGTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACGCTGACTCCAGGAAGTC
 TTTCTGTAAGTCTGACCACCTTTCTTCTGCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCTCTGGCAGAAATGG
 CAGGGGTAATCTGAGCCTTCTTACTCCTTTACCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTCTCTTGT
 TTTGGGATTCAAGAACTGCTGTGACAGACTGTTATTTTTATTAATAAATAAAGGCTTAAAAAA

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FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSILGLFLFQLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAIIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGLSHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPILTRVSGGAALAAQQSYWP
HFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADANNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG
 TGAGC**ATGG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCCTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAAGTC
 ATTTTTTAAATAGAAAAGGATATCATGGATTCCCTTAAAGAAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTCTTCTTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATCTTTCCACTTCATTGGCTCTTTTGGAAATTTGGGCTACCAATCCCCTTGTCTTATGTTCT
 CAGTATCCGTTCTTGTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAAGGCTCTAGGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GTTTCATTAACTCTGACTTTGGCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT
 GTTGAGGCTTGATGGA AAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGGA
 CTGGCTTCCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGCTGTGTTTGTCAACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGCCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGCTGCCAGTGTCATCCTGCGCTCCCAACCCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCCTCCAGACAGGGGCGCGCAGCAGCATCAAGGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTCTTGGCAGCCCCATTCTCTAGTCCCTT
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGC
 TAAATTTGCTACAAATTCATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTCCAGTCCT
 CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCATGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTATGCGGCTCTCCGAA
 TCACACCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCTGCTT
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATTTCTCAGTTTCTGTTTT
 GTTCTCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCCAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCAAGTGAGCTCCT
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

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FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKGRP
FMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAEWLF
INSDFAFDFAFPLLPNTVYVGGLMKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFPQPPWHEQYLFDFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCCTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCGAGA
 AGACCGGGGCACCTGTGGGTTGACAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC
 TACCAGGTCGCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCCACCCCTGGGC
 GAGTGGCATTGTCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGC
 CTCTGGCTCCTTCGTAGCCCCGTGCCGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG
 TGTACAACGCCAAACTGTCCAGGTGAGCCTGATGCTGAACAGCTGGCCCTGTCTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCACCCACAGCTCTGTGCTACTGCCCTTGGGA
 CCCTGGGGACCCAGTGTCTCTGCGCCTGCGTGGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**GA**GGACCCAAGTCTTTCAAGCACAAGAAT
 CCAGCCCCGTGACAACCTTTCTTGCCCTCTCTTGCCCGAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCAAGTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCCTGCGCTGACGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTCTGCTCCTCCGGTTCGCCACCCCAAGCTTCCT
 CTCTAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGCCCCCAAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTCTATGTCTGGATCCAGATGGACTCTGGCCCTTACCCTCCCACTGAGATTAG
 GGTGAGTGTGTTTGTCTGTGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCTCCACACTCTGACTGCTGGCTCCTTCTCCCGAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGTCTTATCTCTCTCCTTAGGCTTCCTATTACCTGGGATCCATGATTCCTTCCCT
 CAGACCTCTCTGCCAGTATGCTAAACCCTCCCTCTCTCTTCTTATCCCGCTGTCCTTATT
 GGCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGAGGAAGATGCCTCTGGAGTTGGATCGGCTGTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACGTATACATAAAATTAATAA

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FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECELVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

[illegible]

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FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGRRS
QWVRNWA V WRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCGGGGCGGGCGGCGCCGCACTCGCTGAGGCCCGACGACGAGGCGGGGCGGGCGGCCA
 GGGCCGAGGAGCGCGGCGGCGAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCGCGCGACGAGCAGGTGGCG
 CGGGCTGCAGGCTTGTCCAGCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGA
 CGGCTGTCTCAGCGAGGGGCGTGCACCCGCTCCTGAGCAGCGCCATGGGGCTGTGGCTTCTCTGAAGACCCA
 GTTCGTGTGCACTGTGGTGGCTTGTCTTCGTGGTGAGTGGTCTGTGCTCAACTTGTCTCCAGCTTGTGCAC
 GTGGCGCTCTGGCCGTCAGCAAGCAGCTCTACCGCGCCCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACAGGACGACGGCCAGGTAAGACGCTT
 TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA
 GCGCTTCGGAGTGTGGGAGCTCCAAGTCTCGCTAAGAAGGAGCTGCTCTACGCTGCCCTCACTCGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGACACCGTGGTGAAGGCTGAG
 GCGCTGTGCGACTACCCCGAGTACATGTGTTTCTCCTGTACTGCGAGGGGACGCGCTTACGAGAGCAAGCA
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGG
 CTTCAACCACCGCAGTCAAGTGCCCTCGGGGACAGTCGCAGCTGTCTATGATGAACCTGAACCTCAGAGGAAA
 CAAGAACCCGTCCTGTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT
 GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACGAGGAGAGGACGCGCTCCA
 GGAGATATATAATCAGAAGGCATGTTTCCAGGGGAGCAGTTTAAAGCTCGCCCGAGGCGCTGGACCTCCTGAA
 CTTCTCTGTCTGGGCCACCATTTCTCAGTCTTCCCTTTCAGTTTGTGTTGCTTTCAGGCGGATACC
 TCTCCTGATCTGACTTTCCTGGGGTTTGTGGGAGCAGCTTCTTGGAGTTCGCAGACTGATAGGAGAATCGCT
 TGAACCTGGGAGGTGGAGATTGCAGTCGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCCAAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCAGAAATTCGAGAGTTGAACCTGTGTAGTTACTGACATGAAAA
 ATTCACTAGAGGTGAACAGCAGATTGTAGCAGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
 TTTCAAGCTTAATGAAAAAAGAAATGAAGGAAATTAACAGCCTCAGAGACCTGGTGGCTGCACCTGACCATCAA
 CATATGCATGATGAGATCCCAAGGAGAGAGAGAAAGGTCAGAAAGATGGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCTAT
 AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTATCTTGTTCAAAGGATCTTTG
 ATCAGATTAAAGACTCATTTCCTCAGAAATCATGGGAGCCAGGAGACTGTGGGATGAACACTGTTGAAGGCAA
 AACCTTCAACTGTAAATTATTGGACTTTTGTAGTCTTAGTGGTCTGACCTCTTGTCTTCAGGACAGTTTTTCA
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCTGTCTTTAGGCCGGGACAGTGGC
 TTACACCTGTAAATCCGACACTTTGGGAGGCCAGACGGGTGGATCATTGGGGTCAGGCTGATCTCAAACCTCT
 GAGTCTGAGTGTATCGCCCGCTCAGCTGCCAGCTCCCAAGTGTGTGATTGCGCGGTGAGCCACTGCACCTGGCCGA
 ATTTCTTTTAAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCTGTGATCCCAAGTAGCTTGGATTGTA
 AACATGCACCACCATGCTGGCTAATTTTTTGTATTTTGTAGTAGAGAGCTGTAGCCAGGCTGGTCTCGATCTCTG
 GACCTCAAGTAGACCACTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
 GCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTATCTTCTTGGGGAAATGTCTGTTCAAGCTTGTG
 CCTTTTTAAATTTTTATTATTTATTTATTTATTTTGTAGACAGGCTTGTCTGTGTGCCAGGCTGGAGTA
 CAGTGGCAGAGCTTGGCTCACTGACGCTCGACCTCCTGGGCTGCAGTGAATCTCCCACTCAGCCTCCCTGT
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCAATTTACCATGA
 TGCCAGGCTGGCTGTGAACCTCTGAGTCTCAAGTGATCTGCGCTGCTCAGCCTGCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCCAAAATTAACACACACACAAAAAACCACTGATTCAAAATGGGCA
 GAGGGGCGGGGTGTGGCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAGACCTGTCTC

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FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVVSGLVINQVQLCTLALWVPVSKQLYRRNLNRLAYSLWSQLV
MLELWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSSLGILYGGK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFVRRLLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCCTTTATTTTAAAGAACTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTCTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTTCTCTTGTCTGTTCCCTGTAAATGGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCATACATGTGGTGCGT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGATAGGCCAGCATTTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTCACTAGGCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAAGGTTGAC
AGAGTGAGACTCTATGTCCAAAAA

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FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop .
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSIQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGRLRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCTACTCTACCTAC
 ATTAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCACCTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGTA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCAATTCCTCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGA
 GGGAAAGGAACCTTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAAGC
 ATCGAGTCTCCTGCATTAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGACGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCCTCCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGGCTAATG
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGST
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGGAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTGTAA

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FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKS VFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCTGTTGGGAGGCGGT
 GCGCCCATGGCGAGGCGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGGATTCATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCCGCGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCGCCCGGAGCTGGGACGCGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
 C**TAG**GGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATGAC
 CCTGAGTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

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FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPFWRGRREQCLPPEDSRLWQYLLSRs
MREHPALRSRLRLTLEQPQGDsMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCsAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCGAGCCGCTACCGCCGCTGCAGCCGCTTTCGCGGCCCTGGGCTCTCGCCGTCA
 GC**ATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCC
 CATCTTTTTCTTTGGCACACAGAAACAGCCTTCTGGGACCCAAAGGACCTGTTCCCTACG
 ACAATGTAAGAGCAAGTACGGGAAGCCAAACAAGAGGAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCTTCGCCAGTGAAGCTCCTCCGACAG
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCCGTACAGCGGTAAACGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACCCCTGCGCTAAGATGTC
 GGTCTCGAAACGAGCCCCAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCG
 AAGAGGAGAACTCGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAGAA
 GGCGCCGTGAGCTCCGACTCCGACTCCAAGGCCGATTCCGACGGGGCCAAAGCCTGAGCCGG
 TGGCCATGGCGCGGTGCGGCTCCTCCTCCTCCTTCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGAAGCGCGGGACGAGGCGGGAGGCGCGAGCTGGAGGCCCCG
 CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 CGGGAGGCCCGAGCGGGCCGACCGGGGAGGCTGAGCGGGGACGCGCGGCGACGCGGGG
 ACGAGCTCAGGAGGAGCATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGT
 CCCCCTCCTCCTGACTCCGAGCCCCGAGGCCGAGCTGGAGAGAGAGGCAAGAAATCAGC
 GAAGAAGCCGAGTCTCTAAGCACAGAGCCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
 TGCGGCCCCGAGGAGAAGCAACAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGACCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTTCAGGTGACCTCTCAGATCCTCCAGAAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA
 GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCCAAGATCGAGGGCGG
 TGCAGAAAGTGAACAAGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGCGGAGGACAAAGCCAGCACCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCCGACGAGGACAAGGAGCACG
 AGGAGGTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCAGAGGGGCACG
 GGGGACTCGGAGGCCCTGGACGAGGAGCT**GA**CGCCCGGGCAGCCAGGCCAGCCAGCCCGC
 CCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTCGCAGGAGCAGCAGAGCAGAACTGTGG
 GAACGCTGTGCTGTTGTATTGTTCCTTGGGTTTTTTTTCTGCCTAATTTCTGTGATT
 TCCAACCAACTGAATGACTATAAACGGTTTTTAATGA

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDG
VMAVTAVTATAASDRMESDSDSDKSSDNGLKRKTPALKMSVSKRARKASSDLQASVSPSE
EENSESSSESEKTSQDFTPEKKAARAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKPPRRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRRELEARRRREQEEELRRLREQEKEKEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNAL EELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKEAV
QKVNKAGMEKEKAEELAGEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSDHLDSVREGPLDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ACACCATTTGAAGAGAACATTTGTTTTCATCATGAATGCTAATAAGATGAAGACTTAAAGCCAGAAGCCAAGA
 TTTTCACCTTTTCTCGCTTTGATGATGCTAAGCATGACCATGTTGTTCTTCAGTCTCTGGCACTTTGAAGCA
 AAAATATTCCAAGACTCAAGCTTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTGGGTTCATC
 AGAAGGAGTGGAATTTTCAAACCTTCTCTTAGATGAGGAAGGCGAGGCTGCTCTTTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTATTGGCCCTGCTGCAAAAGGACCGGTGGGA
 ATTATGTAATAGACTGGGAAGTGGCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACTGGAGCATTTTCACCAATATGTGGGTATATGTATCTTGGAGTCTACAAGGA
 GGAATATTATATTCAAACTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCCTTCGATCCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCGTATTTCCCTGGGCAAGATACTGCATTT
 CACTCGATCCCTTGGGCTACTCATGACCACCCTACATCAGAAGTACATTCAGAGCACTCTGCGCTCAATGG
 AGCAAAATTTATTGGAACCTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTCTTTCG
 TGAATCATCTCAAGAAGGAGTACCTCCGATAAAACCCTCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
 AGGAGGACAAACGAGCCTGATAAACAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGTATGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTATTTACTCCCCACAAGAGATGAAAAGAACTCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAGTGCAGACCATCGTTGGGTGCAAGTATGATGGGGAAT
 TCCTTATCCACGGCCTGGTACATGCTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
 TGATGTCACTGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATAACAGTTGCGAGGAGGACCAAGCTT
 CAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAAGAGATGGCCAGTAGCA
 TGTAAATGTTTCTTGGAAACAGACATTTGGAAGTCTGCTCAAAGTTGTCAGCATTTCAAAGGAAAGTGGAAATGGA
 AGAGTGTAGTGGAGGAGTTCAGAGATTTCAAGCACTCATCAATCATCTTGAACATGGAAATGTCTCTGAAGCA
 GCAACAATGTACATTTGGTTCCGAGATGGATTAGTTAGCTCTCCTTGCACAGATGCGACACTTTGGGAAAGC
 TTGCGCAGAGTGTGTCTTGCCAGAGAGCCCTACTGTGCTGGGATGGAAATCCAGTGTCTCGATATGCTCTTAC
 TTTCTAAAAGGAGACTAGACGCCAAGATGTAAATATGCGCAGCCCAATCAACCAGTGTGCGACATCGAAGACAG
 CATTAGTCATGAACTGCTGATGAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACCC
 TAAATCCCAACAGCAACTATTAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGATTGAAGCCCGGA
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAGGATTCTGGGATGTATACGG
 CAAAGCCAGGAGCACCTTTCTCCACACCATAGTGAAGCTGACTTTGAATGTCTTGAAGATGAACACATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATGACAAAG
 CTACATCCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCACTACTGCGAACAGATGTGGCAGAGGGAAGCG
 GAGACAGAGAAACAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAGAAACGAAATCGAAGACATCA
 CAGACACCTGGATGAGTCCCTAGAGCTGTAGCCAGTACTGAGCAGTACTTCTACTTAAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAAAATTTGCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCATGGAGTGTCTGCTAAGG
 CACAAGACATAATCTGAATAAGACATATGTATGAATATAAGAAAGGGCAAAATTCATTTGAACGAGTTT
 CCAAGAACAAATCTTGCAACAGCAAGTATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
 TGTTTTGAGTTTGGAAATTTATTGTCTGTAATAGTATTGAGCTAAGCAAGCCCGAAATTTGATAGTGTATAAGGT
 GCTTTATCCCTCGAATGTCCATTAAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTCCTATTGAGAACAGCTACCTTTGTTGATGGGAATAAGAGGTGAGACACAAATTAAGACACTCCCATATC
 AACAGAACTTTCTCAGTGAGCCATCTACTCCTGGAGAATGATAGGAATTTGGAGAGGTCGATATTTCTTCT
 TGCCACTGGGTTAAATTTAGTGTACTACACATGATTTACTGAAGGGCAGTAAATGTTTCCCCAGGATTTCT
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTAGTGCTTTAGATATGTTTTTTAGAGTATATACCTA
 GCTCTACAGGACAGAAATGCTTAATAAATCTTTAATAAGTATGGAATATTTTAAATAACAGGAATAACA
 TAATGATGTATAATGCACTCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAGACAGCCAT
 AAATCTGCTGTTTTGGGAAACATCATATCCCATGAAAGGAAGAACAACTCAAAATGAAGTGAAGATGATGTAA
 TGGAGCTCTTTTCACTAGGTTATAAGTAGCTGCCAATTTGTAAATTCATCTGTTTAAAAAAATCTAGATATAACA
 AACTGCTAGCAAAATCTGAGGAACATAAATCTTCTGAAGATCTGAGGAAGTAGACATTTTATTATTAACC
 AATGATATTTCAAGTATATTTTCTCTTTTAAAAAAATATTATCATACTCTGATATATTTCTTTTCTACTGC
 CTTTATTCTCTCTGTATATTTGGATTTTGTGATATATTGAGTGAATAGGAAACAAATATATACACAGCA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTTGTGAATAACAGAACGAGTGTAAATTTTAAC
 AACGGAAGGGTTAAATTAACCTTTTACACTCTTCACTCAACCTTTCTCATCTGCTGAGTAACTCTGTGTAAT
 GTAGTATTGTTTTGTAAATTTAAACAATAAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLILLDEERGRLLLAGKDHFLLSLVDLNKNFKKIYWPAKERVCLCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSACVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYFP
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVLEE
LQIFKHSSIIILNMLSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSSQQA
TIKWYIQRSGDEHREELKPDRIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRRNRHHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCTGGAGCATGCCACC GCCGGGAGCAGA
CAACCTCCCGAGTAAAGCTGGGAGCAGACCTGAAGCTGTTCTCTCAGGAGCCTGGTGTAATTTTCCCCACCCAC
CTCAGCAGTTTCAACCCAGGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAAGCGCTGGGTGGCAAGA
CTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC
GGTGAGGTGGGGGGGACAGGTGTCTATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGCTATGGAGCTACAGAGGGGAGGGAAAGGTATTTTAAAGTTAAACAGTGTGGCACAAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCAGACATAGGTTCAAATTTCTTCTGTGTTCTTCTTCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGAATTCATTTCTCTATCACTAAAGTAGGGCCAAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCACTCAACTAGCAAGTACCAGTCCCATAGTTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCTTCCCAACCAAGTACTGCAACGAGCTGGAGCAGAGGGCGGAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTCGAGAGAGACTCCGCCGGGACAGGTTAGGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAAGGGGCTGGCTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGGCTCAGTGAGGCTCGGCTGCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCTGGCCACAGGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGTATCAGGCAGGGCGTGAGGATG
AGCTGACAAATCAGGAGGGTGAGTGGCTGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCAGCGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTCCCGGACCTCTCCCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTCGCGGGGACAGGCCACAGCATTCCTGGCAGAGCCCTGATACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGTCTTCCCTGAGGGGCACTCATCCGTCTGCTGCCCGGGCCAAAGATGAGGTAGATGACG
CTTCTGAGAGGGAGAAATTTGGGGGCGGTGTGGGGTCTTCCCTCCCTGCTGGTGGAAAGAGCTGCTTGGCCCC
CAGGGCCACTGAATCTCTGAGGCTGAACAGATGTCGCCGTCCTCTCTCTCCAGCTTCTCCCAAGCTTGAC
CTACCTCTGTGTGGATGGGCCCTCTGACCTGTCTGCTGGGACAAAGCCCTGGACTCTCCCTGGGTTCTGTG
ACATGATGGCACCTCTCAGGCCGATGCGTCCACCACCTCCGCCCGGCTAAAGCCCGGAGTCTGGCCACC
CAGATCCCTCACCCTGAAGGCCAGGGAAGCCTTGACCCCAAGTATGCTGCTTCCCTATCTCAAGCTCTGACA
CCACACCATCAATGATCAGGAGCAACAGGCCAAAGAGCTGGAATGCCCTTATTTCCACCTCACTTCAAGGGT
GGAACCTTGCCCTTCCATTTCTAGAGCTGGAACCACTCTCTTTTTCCTATCTATCATCTTAGGACC
GAACTACTACTCTCTCTCTGTCATGACCTATCTAGGTTGGTGAATAGCTGAAATCTCTGGGGCTGGAACC
ATCCATCAAGTCTCTAGTAGTTCTTGGCCCACTCTTCCCCACCTTGGCTCCATAGCACCCCACTCTGGATG
CCAGGTCACCTGGGGTTGGGCTGGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGATGCGAGCAG
CTGTAATGGTCTGAGCGGATTTATTGCAATGAATAAAGGGACAGGAAGGCCAGGCCAGGCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACACAGGCGCAGGGCTGCTCCCACTGCCAC
GCTCTATCATATGAGCGAGGTGTTGGGGAAAGCGGGGAGGCGAGCCTGTTGAGGACAGGGGAGGGAAGAGAG
TGAGGGGCTGTGACCTCTCTCAGGCCCCAGGCTGAGACTGTGCACTCCAGGTGGAAGTAGAGCTGTGTCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCAACCAACCCCTGGCCCTGCCAGCTGTGAG
TCCATCAGCACAATGAAGAGACTTGGAGAAGAGGAAGAATAACACTGTGTTCTCTGTCAAGCTGTGCTGAT
TTTTCCCTCGGGCTCAGGACCTTCCCTACCTCCACCACCAAGGGTTTATAGCAAAGGCTAAGCCTGC
AGTTTTACTCTGGGGTTTCAAGGAGCCGAAGGCTTAAATAGTTTAAAGGTGATGGGAATGAGATTAACCTCA
TTTTAGGGCTCAGGCAGACTCACTCATACTCCCTGCTCCCTGTGTTAGAGACACCTTGAGAGAAGGGGAGGGG
TCAACAATGAGAGACCAGGATAGTGCTCTATCAGTGCCCCAGTAGAGAGCAATAGAGAGCCAGGCTGAGTGC
AGTCTCGGCTGTGTTTTCTTCTACTGGTATCAGAAGTGTGGTTGCTTGGCTGCCATTTGCCCTCTGAGTGG
GCAGGCTGGGCTTGGGCCCTCCCTCGGCCCTCAGTGTGGCTCTGCAAGAGCTCTGGGTTTCCCTCAAGT
CAGAGGGGTTAGGCTGCTGCTGAGTCTCCATCTCTGACTGGGGGCTGGCTAGGACCTGGGCTCTGGCC
TCTCAGGGGCTGCTCTTCAAGTGGAGGATCCTGCTTGGGCTGCCCTGCCAGACCCCTGACACCCCTGCTG
GGTCTGTGCTCCCAACAGAGCCCAAGCTCTGCTGTCTGGGGAGCCATACGGGTGTCTGTGACTCATAGGCT
TCTCAATGTGCTGACCCGACCTTGGAGGGGAGGGAACACTGGGTTTACAGACCAACTCAGAGCTCAGGCTTG
GCCCTCCCTCTGACAGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGTAGGGAGGGCTCTC
AGATTGTGGGAGCAATTGTGAGCTGACTTCTGTGGAGCTCCAGTCAGAGGAAGAGCCAAAGGCCCACT
TTGGAGTCAGTGCGGTACTGCTGGGCCCTACCTCAGCCGCCCTTCCCTGGAGCACTGCCCACTGGCC
TGGAGAACAGTGGTCTCCCTCTCGGGGGGGGCTTTTCTTCTTGGAGGCTCCTGACGGACAGTGGAG
GCTCTTGTCTGGGCTCAATGGATGCAAGGGGCTCGAGAGCCAGTGCATCTGTGATGATGGAGGGGGCT
CGTCTCGAGCTGGAGTGGACTTACCACTGACACAGAGAGGAGGAGTGGAGTTAACTTTCTTCTCTCT
TCATGTTTGTGTTCTTACGTTCTTTTACAGTGTCTTAAACCCAGAGGCCCAATTTTCCCAAGGCCCAAT
TTCTTGTCTTTATCTAATAAATCAATATTAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCPLNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEFPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPSSQSDSNPCGAEPFTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVDGPPAPVLPDGKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDLT

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGCAGGGGAGGCACAGAAAGCGGCCACAGACAGTCTTACAGAGGGAGAGGCCAGAGAAAGCTGCAGA
 AGACACAGGACGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGACTTTGGAGAAGCCAGACCCCTGG
 GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGCTCTCAGCCCTCTCGAAAACCTTTGCC
 TCTGACCTTTGGCAGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCCTACAGCGGCTCATCTCCCTCCAGAGCTCAGATACAGTGCCTATGTCCAGACAGGCTCGATCCGGGAGAGGG
 CTTGGAGGGGCGTGGCTGTGGGAGGCCAACCTGCCTCGCTGCCATTTGCCGTCTCTCTGGCTGGTGTG
 GTGCTTTCTGCTACTGCTGGCTCTCTCTGCCCTCAGCCCGGCTGGCAGGCCCTCCCCGGGAGGAGGAGAT
 CGTGTTCACAGAGAAGCTCAACGGCAGCGTCTCTGCCCTGGCTCGGGCGCCCTGCCAGGCTGTGTGCCGCTTGA
 GGCTTTTGGGAGAGCGTCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTTCAGAGGGCTCAGAGTGCAGTA
 CTTGGGCGAGGCGCTCGAGACTGCTGGGTGGAGCAGAGCCTGGCAGCTACTGACTGGACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTCTGCAGCTGGGATGGGGAGCCCTGTAGGCGTGTACAATATCGGGGGGCTGAACCTCCA
 CTTCCAGCCCTGGAGGGGAGGCACCCCTAACTCTGTGGGGAGCTGGGGCTCACATCTACGCCGGAAGAGTCC
 TGCCAGCGGTCAAGGTCCATGTGCAACGTCAAGGCTCTCTTGGAAAGCCAGCCCAAGACCCGAAGAGCCAA
 GCCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCACCGGTGC
 GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGAGCCAGGCCCTTCAAGCACCCAGCATCCGCAATCC
 TGTCACTTGGTGGTGACTCGGCTAGTGATCTGGGGTCAGGCAGGAGGGCCCCAAGTGGGGCCAGTGTCTGC
 CCAGACCTTGCAGCATCTGTGCTGTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCATTTGA
 CACAGCAATTCGTGTTTACCCGTCAGGACCTGTGTGGAGTCTCACTTGGCAGACGCTGGGTATGGCTGATGTGG
 CACCGTCTGCAGCCGGCTCGGAGCTGTGCCATTTGTGGAGTATGATGGGTCCAGTCAAGCTCTCACTGTCTGCTCA
 TGAACCTGGGTGATCTCTTCAACATGCTCCATCAACACTCCAAGCCATGAGCTGTTGAATGGGCTTTGAGCAG
 CTTCTCGGCATGTATGGCCCTGTGATGGCTCATGTGGATCTTGAAGAGCCCTGGTCCCCCTGAGTGTGCCCTGT
 CATCACTGACTTCTTCAGCAATGGCTATGGGCACTGTCTTTAGACAACACAGAGGCTCATGTGCACTGTCCGTG
 GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTGGGGCCGAGTCAAGCCATTTGTC
 ACAGCTGGCCCGCCCTGTGCTGCCCTCTGCTGCTTGGCCACTCAATGGCCATGGCATGTGCCAGACAACAA
 CTGCGCCTGGGCGGATGGCAGACCGCTGGGGCCCGCACAGGCCTGCATGGTGGTGCCTGCATCCATGAGGACA
 GCTCCAGGACTTCAATATTTCCACAGGCTGGTGGTGGGGTCTTGGGAGCATTGGGTGACTGCTCTCGAGACTG
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
 CCGCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAAGCTGGCTGAGCCCTTCCGCGAGGAGCA
 GTGTGCTGCTTACAACACCGCAGCCAGCTCTTCAAGAGCTTCCAGGGGCCATGAGTGGTCTCTCGCTACAC
 AGGCGTGGCCCCCGAGGACAGTGCAAACTCAGCTGCCAGGCCGGGCACTGGGCTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTCTCCCGGACAGCTCCTCGGTCTGTGTCAGGGCCGATGATCCATGCTGG
 CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGATGGTGTGCGGAGGGGACGGTCTTGGTTCGAC
 CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACACAATGTGGTCACTATCCCCCGGGGGGCCACCCA
 CATCTTGTGCGGAGCAGGGAACCCCTGGCCACCGGAGCATCTATTGGGCTGAAGCTGCCAGATGGCTCCTTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGCGAGTCAGCTTGCCGTA
 CAGCGGGCCCATCGAGCTCAGAGCACTGTCAAGGCTAGGGCCATGGGCCAGCTTTGACACTGCAAGTCTCT
 AGTGGCTGGCAACCCCGAGGACACAGCCTCCGATACAGCTTCTCTGTCGCCCGGCCAGCCCTTCAACGCCACG
 CCCCACCTCCAGGACTGGCTGCACCCGAAGAGCAGATTTCTGGAGATCTCTGCGCGCCCTCGGGCGGCGAC
 GAAATTAACCTCACTATCCGCGCTGCCCTTCTGGGCACCGGGGCTCGGACTTACTCGGGGAGAAGAGAGACTT
 GTGTTGCTGCCTCATGTGAAGTCACTGGGAGGGGCTGGGGCTGAGACCTGCCCTCTCTCTGCCCTAAT
 CGCGAGGCTGGCCCTGCCCTGGTTTCTCGCCCTGGGAGGCACTGATGGTGTAGTGGATGGAAGAGGGCTGACAGC
 AGCCCTGACCATTAAGTGCCTCTGCCCTGCGGTACAGAGGAGGGGAGGAGGAGGGGCTGGGCC
 CAGTTGTATTTATTTAGTATTTATTCACCTTTTATAGCACAGGGAAGGGGACAAGGACTAGGGCTCTGGGGA
 CTTGACCCCTATAGCCCTCATAGCCCTCAGCTGGGCTAGGAAATCAGGGTGGTGGTGTAGTATTAAGTGGTGGT
 TGTGTATCGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACACACCTGTCTGCTTTCCCT
 TCTCGAATTTTATTTTTTTGGGAAAGAAAGTCAAGGTAGGGTGGGCTCAGGAGTAGGGATATCTCTTT
 TTTTCTTTCTTTCTTTCTTTCTTTTGTGAGACAGAATCTCGCTCTGCTCGCCAGGCTGAGATGCAATG
 GCACATCTCGGCTCACTGCACTCTCGCCTCCCGGTTCAAGTGAATCTCATGCTCAGCTCTGATAGTACTG
 GGATACAGGCTCTGCCACACGCCAGCTAATTTTGTGTTGTGTTGGAGACAGAGTCTCGCTATTTGTC
 ACCAGGGCTGGAATGATTTTCACTCACTGCAACCTTCGCCACCTGGGCTCAGCAATCTCTCGCTCAGCCTCC
 CGAGTAGCTGAGATTTATAGCAGCTACACCAACGCCCGGCTAATTTTGTATTTTATGACAGAGCGGGTTTAC
 CATGTGTGGCAGGCTGGTGTCAACTCTGACCTTAGGTGATCCACTCGCCTCTATCTCCCAAGTGTGGGAT
 ACAGGCGTGAAGCAGCGCTGGCCAGCCGCACTAATTTTGTATTTTATGAGAGAGAGGCTTTCACATGT
 TGGCCAGGCTGCTTGAACCTCTGACCTCAGTAACTCAGCTGCCTCGCCTCCCAAGTGTCTGGGATACAGG
 TGTGAGCCACACGCCCGGTACATATTTTTAAATTTGAATTTACTATTTATGTGATCTCTTTGGAGTCAGACG

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit.1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNQSVLPFGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPPELLGGAEP
 GTYLTGTINGDPESVASLHWDGALLGVLRGAELHLQPLEGGTPNSAGGPGAHLRRKSP
 ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKKRYLLTVMAA
 AAKAFKHPSIRNPVSLVTVTRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
 NSKPCI SLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCCLHMDQLQDFNI PQAGGWGPWGPWGDCSRCTCGGGVQFSSRDCTRPVPRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPODQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFKDKMVCGGDG
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGATTTACATGGAATTGATCCTGTG
ACCAGAAGTAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACTTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGATGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAAGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT
AATAAATGCATGTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILVLFWGSKHFWEVVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPA NEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEI F D P M L D E R G Y C C I Y C R R G N R Y C R R V C E P L L G Y Y P Y C Y Q G G R V I C R V I M P C N W W V
ARMLGRV

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCC**ATG**GCCAGCAGCGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGGCACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCCTGCTTTGCCTGTCTGCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGGCC
 CAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGCGGGACTGTC
 AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTTATGAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLTTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLCLSCQ
 DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCTCAGGAGCGCTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCGGCAGGGCGGGCGGCCAGGAT**CATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCTCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
GCATGGGTGGGATGGTGAGACTGTTTCAGACCAGGTACACATTTGGTGGCGGCTCTGTTCTGTG
GGCTGGGTGCTGGAGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAGAAGAAACCACTACAAAGCCGTTTCTTATCATGGCTCAGGCCACAGTGTTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGAGAGCTCACCCAAAA
AACAAAGGAGATCCCATCTAGATTTCTTCTTGTCTTTGACTCACAGCTGGAAGTTAGAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCTCTAT
TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAACACTTACAGAGAA
GAAGCAATAAGAGAAAAGATATTGTAATCTCTCCAGCCATGATCTCGGTTTTCTTACACTG
TGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACTTTCTACTG
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
TTAAGTCTCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATCCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
AGGTTGGGGCTGCAGTGAGCCATGATCACCACTGCACCTCAGCCAGGTGACATAGCGAGA
TCCGTGTCTAAAAAATAAAAAATAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
ACTAATCTTTAA

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FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYSPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACTCATCCTCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGGCCCTTCATTGAAAACAACATCGTGGTTTTTGAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAGAGCAGTAGTACCTA
 GATACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTTATCACACCGGAAAGAGTCAACG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTACAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTTAAAAACAGCTTAGGGATTAATGTCTCCATTATATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAGGAAATGAATGGCTTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATGCTCTTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAATAACATTTTTTAAACGCAGATATTTTGTCAGGGGCTTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAATTTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTAGTTTTACTAAA
 ATCTGTAATAACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA
 TTAATAAATGTACATTTTTCTAATT

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FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**AT**GGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACC GGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC
 CAAGTGTAACACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCACTCTGGGA
 TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTCTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCCTCCCT
 CTAATTGGGCTGGGCGGCCTCAGGCCCTTTTGTGTGGGTGGGGGGTTGCTGTGCTGCACTT
 GCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCTT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**G**AGCTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
 CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTTACTGAGGATATTTAAATTCATTT
 GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
 ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
 CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCTCCCAAGAGTTCCTGCTGTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCTCCGTCCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCTCCCTCGTCTCACCCCTTTTACACTCACATTTTATCAAATAAAGCATG
 TTTTGTAGTGCA

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FIGURE 190

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAIISRGPSSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAAGTCTTCAAAGTAAAGGCAATGGCATTATATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTG**GATGA**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCGGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATAACCTTCTGGGAACCTCAGGAGTCCCTTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGCT**TAA**TGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
 GAACCTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCAATCGCTGCTCCAATTTTCATATTCIAAATCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLI PVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

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FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCACTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNQVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCCTGCCCTCCCCGCGCGGCCTGCTGTCTCGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCAGGTTGC
AGCAGTGGTACCAGCAGTTTCTTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TA**ACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY**Signal peptide:**

amino acids 1-30

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FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCTCTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCAGCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCAAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
CCCCGGACTCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCAACCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
GGACCTTGCTCCCCGCGCGCGGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCCGCGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCGGGGGCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCCGTTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCGCCGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAAAAAA
AAAAAAA

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FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPCCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFFLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCAGGCTCTCAGAGAAGATCAGCAGAAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
 TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGGTCAGCAGC
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
 TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCG
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGACCCGTG
 AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
 CTTTCATGTTATTTTCTTCCCTTCCCATTACAACATAAACTGACCAGAGCCCCAGGAATAAA
 TGGTTTTCTTGGCTTCTCTTACTCCATCTGGACCCAGTCCCCTGGTTCTCTGTCTGTAT
 TTGTAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

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FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACC
 CCAGTTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGTAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCCTGTGGTTTCTGATTGTAAGTGGAAAGCAGGTCTTGACACACGC
 TGTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCCTGATGATGGTGGCGATGT
 TGCACCTCCCCACACACCTGCACCAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCTCATCAAGCAGCCAAGGAGGACAGGATAAGGAAGCCCCAAGAGGAGACTGGG
 GGCTGATGAGGACGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCCCTGGACCCAC
 GTGGCTCCAGGAGGCATCAGTGCCCGCATCCCCCTCCAGAGGGCTGCGCCGAGGTGCGG
 CACCCACTGTGCTGTCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTACATCTCTG
 TTTCCATGATGAGGCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGAGAGGTGGTGGCCATGCTGGGGGCCACCAAGCCAGCCGGGATGTGCTCGTCT
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCACGCTGGGGTGTGGACTGGAAGCTGGATTTCCTAGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCTAT
 TCCCCCTCGACAGGAGGCCACCCCTGAGGAACAGGGTTCCGATTGCTGAGACCTGGCTGGG
 GTCAATCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGGAACGCTTCAGCTGCAAGGAGACTGGGTTGTCGGACATTCCTCAGT
 TTTCTGGCTAATGTCTACCCCTGAGCTGTACCATCTGAACCCAGGCCAGTTTCTCTGGA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAAG
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGTGTGTCAGGCAGGAGCAGGT
 GATTCTCAGAACTGCACGGAGGAGGCCCTGGCCTCCACCAAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAA
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAGAAAGCCGCCAGCAGTGGCGATTTCACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAGGAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCATGAAAGAAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTCATTGACTGCGCTGCTTA

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FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIP LQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQQLKSALSEYVAR
LEGVKLLRSNKR LGAIRARMLGATRATG DVLVFM DAHCEHPGWLEPLLSRIAGDRSRVVP
VIDVIDWKT FQYYPSKDLQRGVLDWKLD FHW EPLPEHVRKALQSPISPISRPVVPGEV VAM
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGH IYQNQDSHSPLDQEATL
RNRVRIAETWLG SFKETFYKHSPEAFSLSKAEKPCMERLQLQRRRLGCRT FHWFLANVP EL
YPSEPRPSFSGKLHNTGLGLCADCQAE GDILGCPMVLAPCSDSRQQQY LQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQH WDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

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FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCTCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAGATCACGTGCGGCAAGTCTGCTGGCACTG
 CACCCCGACCCACCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGAGGGGACCCCACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTCAGCCCCCTCATGGGCTCGCAACCCCAACCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGGCGCCATT
 CTGTTCGGGGGCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCAACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGCAAGAGGGGAAGGCAAC
 TTAGCTTTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTGTGAGGAGGCAGGGCGTGGC
 CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTT
 CTTCTCCAGTCTCTCAGGATCTGTGTCCTATTTCTCTGCTGCCATAACTCCAACCTGCCCC
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTCCCCCTTCTATTCTGGCCCTACCCCTTGGTTCCTGACTGTGCCCTT
 TCCCTTCTCCTCTCAGGATCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGGAGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCATCCCACTGAGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGCACACCACCCGGAACACTCCCCAGCC
 CCACGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACACTCACCTCCACCTTAC
 AGGCATTTCACACGCTCCTGCACCTCTCCCGTCCATACCGTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTTCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCGTGATGTTGTGGTGG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCCGAGCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATG
 TCTGTCCTCATTCACACCAATTTGTTTCTCTGTCTTCCCATCCTTACTCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
 CTGCTAAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCGCTGCTGCATCATGAGAA
 AGGGAACCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTGTCTGTCTCTGGTG
 TCTGTGTGTGTCATTTCTGGAATTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCAGCCCT
 CCCTTTGGGCCTCCCTAACCTCAGGCTGCCAGGACCGGATCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCTCCAAGTCTACCCCTTCCCTTCCCGGACTCCCTCCTGTCCCCTCCTTT
 CCTCCCTCCTTCTTCCACTCTCCTTCTTTGCTTCCCTGCCCTTTCCTCCCTCCTCAGGTT
 CTCCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTCTTCTTCTTGTGGTGATCATCTGAATTACTGTG
 GGATGTAAGTTTCAAAATTTCAAAATAAGCCTTTGCAAGATAA

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FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
 CATCCTGTCTGGCCCTGCGCATGGCGTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGGT
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGGCCCCGTGGAGAGCACAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
 GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGGTGCTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA
 GGGGCCGCGCCCGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 207

GGCCGTTGGTTGGTGC GCGCGCTGAAGGTTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCTCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACAGATGATGGATCAGCTGTACAGGGGAAGATGTACTTCC
CCGGGTATTTCCCAACAGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCGGGGACCTCCCCCTAAAGTAGCCCC
CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCCTGAAGTTTGTCTCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACATACATGAAAACAGGCCGCTCAT
CGACTGTCAGCACCGCTGTGGCTCTTCCAGTACGAGACCATCTCTGCAACAACCTGCACAG
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCTTCCAC
CTGGCTGTCTCGGGTAGGGCGGGGCCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGTCTCTGGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCAGAGCTGGCTCCCTCAGCTCCACGCTCCTAGAGGGGCTCCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTCTTTCTCCCTCAAAG
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCTAAAGGGTCCCCATAGGGTCTGGTTCC
ATCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGACACGAGCATGAGTGAAGGCCGC
CCTGACCTGGACTTCAGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGCTAGGGGGTCTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCAGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCTTGTGAGTGACCCAGAGAAGGAGGCGCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACAGCGTGCCGCGGCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTCTGGATGTGGCCACATAGGACCACAGTCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGAGGGGTGGGGACATGGAGAGTGTAGGCAGCCTCGTCTCC
CCGAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGCGGAGACTCAGCTGGACAGCCCCCTGCCTGTCACTCTGGAGCTGGGCTGTGCTGC
CTCAGGACCCCCCTCTCCGACCCCGACAGAGCTGAGCTGGCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGACAGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

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FIGURE 209

AGCAGGAGCAGGAGAGGGGACA**ATG**GAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGTGCGC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATATACTCCA
 TAGCATGGTGCAAAAATTCACAGGCGTGCATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG
 AATTTAGAGACGGAAGACATTGAAAGCATTGATGCCACCAAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCTAAGTGAAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAGGTGGAACCT**TGA**ACTTCTCCTTGGAACATACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGTCACACACGACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCATCTGTAAACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCTATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTCATAAGCACATGTCGCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACCTCAGCAGAAATAGACCATGTGAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

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FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAVEKSSDGPAAQEPTWLTDPAAEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGCGCGTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTGCTAGAAAAAGAGAATTTGGCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTTGTACCAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAAGATGTGT
 ACAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGTCTGTTTTGTACTTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTAGAAAACATTCCTTTACCATCATTTAGAAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGCTTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
 AAATGTGTCATATCAATTTCTGGATTCTAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCATTCTATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

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FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGGVYLGNYPPFKDRISWAGDLDDKASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCSSTSESLSPVKQAPRKSPSDTEGLVKSLPSSGSHQGPVIYAQLDHSG
GHHSKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGGCCCCGGCGCAGTCCCCCGGGCCCCGACCCTGAGGCG
 TCGCCTCTGGCCGAGCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
 GCGGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACC GTTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAACAGATTACTGATTTCCTTAAAGTGAATTTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTGGA
 CTATATGCAGAAAAATATTCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAATAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAA

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FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop .
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEKEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCTGTGACAGCGGCAGCTCAGCGAGGAGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTGCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGGCCAGAAGGCCAAGAACCCCAAGGAGCAGAAG
 TCCTTCTTCGCGCAAATACTGGATGTACATCATTCCCGTCGTCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGCTCACTTGATACGTTATTTCAGAAACCCAAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAACTGTCCCCAGATCGACACGCAAAAAAAAA

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCGAGACCGGGGCAGCAGGTGCTCCGGGGGCCACCC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCAGCTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCACTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGACATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTACTCAACTGTTCCGGGTACCTCTGCACTCACTGGCTTGCCCTAGGGCT
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGATTTGCTCTG
 CTGTCATGCTGATGGCTCTGCTGGCAGTGGTGGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGCTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGACTGGAAAGAAGTGGCCAAAAGTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAACACTTTTAAATGATCAAAAAAAAAA

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FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLGLTIQALFESVIFIFVFLWTFVLDPHGAPLGIISSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSFLMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
 EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
 ELRVSPSTEOPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

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FIGURE 219

GCGACGCGCGGGCGGGCGGGCGAGAGAAACGCGCGCGCGGGCCGGCCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCTCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTACAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGGTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCACCCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGGT**TAGA**AGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGTCTAGGCTGAAAGGGAAGCCACACCAGTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

[illegible]

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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

CTCGCTTCTTCTCTTCGGATGGGGGCCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAAACCAGACGCCAGTACAGGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACTGGGCGAGGGAAGATGTAT
GGCCCTGGAGGAGGCCAAGTATTTACGACCACCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGCTGTAGGCTTCTCTCTGGTGAAGAGTGTCACAGGTGAAACTTGGAGACTCTCTGGG
ACGTGAAACTGGGAGCCTTAGTGGTGGGAATACCAGGAAGTACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCTACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTCACCCGTGGGTGCGTTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAAGTACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

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FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFQAFLRGMVMTSKDRIFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

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FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAAATACATCATGTTTTTCGATAAGAAGAATTTGAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTCTTGGAGTGTCTGGGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCTGCGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCTGCAACTGGCCCCTAAGCCAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTTGTCCCTTCGTATATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAATTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGAAATAAAATCAGTGTCTATAG
 GACAGACCTGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTGTAAACTGGCTG
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTATCTGTGCGAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATCGAGTGAAGAACTACAGCATCTGTGCCAAAGACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCAGGCGCAAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGTTATCTACGTGTCTATGGAAGCGGTACCTGCGAGATGAAGCAG
 CTGCAAGCGCGTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAT
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAATAAGTGGTGTCTTTATTGAACCT
 TGGTGACTATCAAGGGAAACGCGATGCCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCCTTGTCCGTTTTAGTGCATTATAAATAGGTGCATTTTCCCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAACAATGTAAGCTTGAACCTCCGTTTTAAATATAA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCGATTGTGTTTTAAGATAAAACT
 TCTTTCATAGGTAAAAA

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FIGURE 226

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCGKMGVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNLALEFPRLVSLQONLYQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDSENKLTFIGQEILDSWISLNDISLA
GNIWECRSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADAHISFHKKIAGSVALFLSVLVI
LLVIYVSWKRYPSAMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCTCTAAGTTGACTGCTCTT
TAAATATGTCTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAATGTGTGT
AAATTATAATGACCAACACCTTAATGGTGCTGATATCTGGATCCTCTGCTGCTGTTTTGG
TGGCAGCTCTTCTGTGGAGCTGTGGTCTCTGCTCCAGTGCTGCTGAGGAGACCCCGA
ATTGATTTCTCACAGGCGACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACGTGTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTTCCA
AAACATCAAAATTTAGGAATGCTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCTATATA
GTCTGAGGAAGGACAATTGCAAAAAGAATGGATGTGGAAAAAATTTGGTCTGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGAATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAAATTAATGCTTCTCCACTAGTATCCAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCGAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGAGCTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTTCCTGAGAGCCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAAACCTCATCAGACATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

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FIGURE 228

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop .
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGCGCGACCGTGACGAGAAGCCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTCTTTTTTTTTTCAAGCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTCTTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTACTGCACATATACTTTTCAACAACCAAGACATCAAGCAGGTGTCAGATT
 ACGTGAGCAAACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAGA
 ACACAGTGGATGTCGAGAACGGTGTCTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGTAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTTACAATAAAAGCTCTACACATTTTCAAGGAGATGCTGGATTCAATGGAAC
 TCTAATCTGTACATAAAAATTTTAAAGTTATTTGTTTGGCTTTCAGGCAAGCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTTC
 ATTTCTATAACACATTTTATTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCATTGTTGTTCTCAATAGATGTAAGTCTGTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAAATTAAGCAGAGAAAAGGAAATATAATGTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACATATCCTTCAGAATAACTGA
 AGGTAAATTATTGTATATTTTTAAAAATTACACTTATAAGAGTAACTCTTGAATGGGTG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAAGTT
 GTAAACTCTAATCTTATACCTTATTGAAGAATAAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAGTTTAACTCTTGAGTGTCT
 ATGTATCAGGAAAGCACATTTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTACATTATATTTATATAAGAGTATC
 CTTTATGAAATTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAAATAAAGAACATTTAAAAATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCAGAGGAACCCATATCTTGGGTAATCTAGTATATAAACAAATTACTTTTAT
 TTAATTTCCCTTGTAGCAAACTAATTGCCACATGGTGCCCTATTTTCATAGTATTATT
 CTCTATAGTAACGTCTTAAGTGCAGCTAGCTTCTAGATTAGACTATATAGAATTTAGATAT
 TGTATTGTTGCTCATTATAATTGCTACCACATGTAGCAATAATTAACAATTTTTATTAATA
 TAAATATGTTGAATATTGTTTATCATGAAGACAGATTTCCAAATCTCTTCTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTNKRITNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCGGGGCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAAACCGGCCATGCT
 TCCCGGGTGCCAAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCGGTGCCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCGGGGT
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCC
 TTCTCCGCGCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCTTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGCTGCTTCACGACGCACAGTCAGGGCGGGCCTACACGTGGACCTCTCC
 CACAACCTCATTACCGGCTCGTGCCCCACCCACGAGGGCGGGCTGCTGCGGCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCGGTGCCCAACCTCCGAGACTTGCCCC
 TGCGCTACCTGAGCCTGGATGGAAACCTCTAGCTGTCTATTGGTCCGGGTGCCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCGGTGAGCTACCGGGCTGCAGGTCTTGACCTGTCCGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTTAGGCCCTGAGCTCCCTGCAAGGAGCTGGACCTTTCGGGCACC
 AACCTGGTGCCCTGCTGAGGCGCTGCTCCTCCACCTCCCGGAGCTCAGAGCGCTCAGCCT
 GGGCCAGGATGTGCGGTGCCGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCGTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCTT**TGAC**AAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGTGCCTCAG
 GTCCCGAGTAACCTATGTCAATGTGCCAACACAGTGGGGAGCCCGAGGCCATGTGGCA
 CGGTACCCACAGGAGTTGTGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCTCTGCTTCCCTTCCCCACTTATCCCCAAGTGCCTTCCCTCAT
 GCCTGGGGCGGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCCTTCTCATGTGAC
 AGATGGGGAAACTGAGGCCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCGGACCCCAATGCACCTTTCTTGTCTCCTCTA
 ATAAGCCCCACCTCCCCGCTGGGCTCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGCAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
 GTGGGCTAGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGACACTTTGGTT
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACCC
 CATTTTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCACTTCTGGAGCCTCA
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC
 CTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGTCTGCCGACCCATGCTATGCT
 TCTACCCCGAGGCATCTCAGCTTCCGAACCTGGGCTGTTTCCCTTAGTCTTCAATTTTA
 TAAAGTTGTTGCTTTTAAACGGAGTGCTCACTTCAACCGGCTCCCTACCCCTGCTGGC
 CGGGAGTGAGACATGTCAATTTGTAAGCAGAAAAAGTTGCTTGTTCATTTTGTAAAT
 ATTGCTCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTTGCTAGC
 CCATCATCTATAACCGGTCTTGATTAAATAACACTATAAAAGGTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAAGLGGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCAAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCTCCCA
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTACAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGTTATTCAATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTGATGGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

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FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCTGCCGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGCCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACGACCTAGTGAAGGTTGAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTCGTGGTGACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT
ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTGATGAGTCTATATAAAGGCTTTTTTACCATCTGGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTAA

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FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

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FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGCGAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTTCTGTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAATAGTTTTGTTTCTTACATTTTTATGTTT
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGTCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTTGGATAATGAGTATCAGTTTTTTATCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
 AAAAAACAAAAATTAGCCAGGCATGTTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
 AAAAAATATTGTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

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FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAAAGTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTGCGCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGTCAGGTGTGCTTCGCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTCTGGTGG
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
 GGGAGTTCTACGAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAGCCCTTTGAGCAGTTCCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAAGTGTGCAGGTCTTGCACGC
 TGTGTGCGCCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGGTGTCTTTCGTACGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGTTTGA

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FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
 DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKD
 LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
CCAGAAACCCATGATACCTACTGAACACCGAATCCCTTGGAGCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACACTCAGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATTCCCAGTCCC
CTGCACCCCTTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
TGGTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
GCCTCTTACCTTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
GACATTGACCCCTGATTTGCTGTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCCCTACCCCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
CCCAGGGGGGTGAGAACACCCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
ATTATGACTCTGATTCTTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCCTCCCTTCAAGCTAAGAG
AGCTGTCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGTCCCAGATTTCAATGGAACAGCT
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
ACTACCAGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTTGCTTCTTTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGCGAAGAAGAGGCTGGAAAACCGAA
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATATAAATTCTCTCAGATACCA
TGGATGTGGATGACTTCCCTTCATGCCATCAGGAAGCCCTCTAAAATGGGGTGTAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTTGGACATCTCTTAGAGAG
GAATGGACCCAGGCTGTCTTCCAGGAAGAAGTGCAGAGCCTTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
GAAGTTTGGGATATACCCCAAAGTCCTTACCCCCCTCACTTTTATGCGCCCTTCCCTAGATA
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
TATTTGGAATTAAGTTCTGACTTT

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FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS VVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

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FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPPIFVTQLGAQGTILSSEE
LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSIPAGGAGVNPATQGTAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCCGACGGGCTCCGCGGCCCTCC
 TGCTGCTCTGTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCTGGACACCCAACACAAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACACIGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
 GGTTCATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTGGAATATGTTGTGGTCTTTTGTTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

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FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop .

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSR IIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217